GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 9, 2004, 01:42:24 ; Search time 799.247 Seconds
(without alignments)
5206.064 Million cell updates/sec

Title: US-09-963-827B-3
Perfect score: 96
Sequence: 1 gggagagaggaagagggaug.....cgauaguacuggaucccccc 96

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 2199298

Minimum DB seq length: 0
Maximum DB seq length: 200

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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8: gb_pl:*
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10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
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34: em_htg_pln:*
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36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	23.8	24.8	138	9	HSA306918	AJ306918 Homo sapi
	2	23.2	24.2	78	1	HALTRMI	K00307 Halobacteri
	3	23.2	24.2	78	1	HCMET	X03199 Halobacteri
c	4	23.2	24.2	91	9	AY006113	AY006113 Homo sapi
c	5	22.8	23.8	99	1	AB059449	AB059449 Unculture
c	6	22	22.9	181	11	AB059200	AB059200 Sus scrof
c	7	22	22.9	187	11	AU046875	AU046875 Rattus no
	8	21.8	22.7	108	6	AR141692	AR141692 Sequence
	9	21.8	22.7	108	6	AX638750	AX638750 Sequence
	10	21.8	22.7	109	6	AR141696	AR141696 Sequence
	11	21.8	22.7	109	6	AX638754	AX638754 Sequence
	12	21.8	22.7	133	6	AR141694	AR141694 Sequence
	13	21.8	22.7	133	6	AR141698	AR141698 Sequence
	14	21.8	22.7	133	6	AX638752	AX638752 Sequence
	15	21.8	22.7	133	6	AX638756	AX638756 Sequence
	16	21.8	22.7	146	6	AR141693	AR141693 Sequence
	17	21.8	22.7	146	6	AR141697	AR141697 Sequence
	18	21.8	22.7	146	6	AX638751	AX638751 Sequence
	19	21.8	22.7	146	6	AX638755	AX638755 Sequence
	20	21.8	22.7	171	6	AR141695	AR141695 Sequence
	21	21.8	22.7	171	6	AR141699	AR141699 Sequence
	22	21.8	22.7	171	6	AX638753	AX638753 Sequence
	23	21.8	22.7	171	6	AX638757	AX638757 Sequence
	24	21.6	22.5	78	1	HMTRNMET	X01222 Halococcus
	25	21.6	22.5	78	1	SATRNMET	X01223 Sulfolobus
c	26	21.6	22.5	89	9	AY006273	AY006273 Homo sapi
	27	21.6	22.5	191	9	HS78B11F	Z66142 H.sapiens C
	28	21.4	22.3	107	6	AR184444	AR184444 Sequence
	29	21.2	22.1	149	8	AF328872	AF328872 Euterpe e
	30	21	21.9	124	9	HS1C7R	Z60309 H.sapiens C
	31	20.8	21.7	100	11	G43550	G43550 WIAF-2413-S
	32	20.8	21.7	138	10	MMA4LDH5	X02524 M.musculus
	33	20.6	21.5	88	6	AR141690	AR141690 Sequence
	34	20.6	21.5	88	6	AX638748	AX638748 Sequence
	35	20.6	21.5	91	6	A11877	A11877 Nucleotide
c	36	20.6	21.5	91	6	A11878	A11878 Nucleotide
	37	20.6	21.5	129	6	AR141702	AR141702 Sequence
	38	20.6	21.5	129	6	AX638759	AX638759 Sequence
	39	20.6	21.5	141	9	HUMTGMIM	M10957 Human initi
	40	20.6	21.5	167	6	AR141703	AR141703 Sequence
	41	20.6	21.5	167	6	AX638760	AX638760 Sequence
c	42	20.6	21.5	187	6	AX333319	AX333319 Sequence
	43	20.4	21.2	77	1	TATRNMET	X01221 Thermoplasm
	44	20.4	21.2	156	6	AX181678	AX181678 Sequence
	45	20.4	21.2	180	6	I76096	I76096 Sequence 4

ALIGNMENTS

RESULT 1
HSA306918/c
LOCUS HSA306918 138 bp DNA linear PRI 04-JAN-2002
DEFINITION Homo sapiens partial SRCRB-S4D gene, exon 7.
ACCESSION AJ306918
VERSION AJ306918.1 GI:18073567
KEYWORDS SRCRB-S4D gene; SRCRB-S4D protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Padilla,O., Pujana,M., Lopez,A., Arman,M., Vila,J., Gimferrer,I.,
Places,L., Vives,J., Estivill,X. and Lozano,F.
TITLE Cloning of a new member of the SRCR-SF

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  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 138)
  AUTHORS   Lozano,F.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-APR-2001) Lozano F., Hospital Clinic, Servei
            d'Immunologia, Villarroel 170, Barcelona 08036, SPAIN
COMMENT     3' end of intron 6 from bp 1 to 31; 5' end of intron 7 from bp 109
            to 138.
FEATURES             Location/Qualifiers
     source          1. .138
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="7"
                     /map="7q11.22-23"
     gene            31. .108
                     /gene="SRCRB-S4D"
     exon            31. .108
                     /gene="SRCRB-S4D"
                     /number=7
                     /usedin=AJ306912:s4d_mRNA
                     /usedin=AJ306913:s4d_cds
ORIGIN

  Query Match             24.8%;  Score 23.8;  DB 9;  Length 138;
  Best Local Similarity   45.3%;  Pred. No. 2.6e+03;
  Matches   34;  Conservative    9;  Mismatches   32;  Indels    0;  Gaps    0;

Qy         13 GAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAG 72
              ||||| :| |  |: :||||       |:| |: || |  || |  | |:| :    | |
Db        126 GAGGGCTGAGCTCTTTACCGGACGGATCTGTCTGCCAAGCCCAGTCCTCTCTTGTGGCTG 67

Qy         73 AGGUCGAUAGUACUG 87
              |||  |  ||: |:|
Db         66 AGGATGGCAGTGCTG 52


RESULT 2
HALTRMI
LOCUS       HALTRMI                    78 bp    tRNA    linear   BCT 15-APR-1994
DEFINITION  Halobacterium volcanii initiator Met-tRNA-i.
ACCESSION   K00307
VERSION     K00307.1  GI:174729
KEYWORDS    transfer RNA; transfer RNA-Met.
SOURCE      Haloferax volcanii
  ORGANISM  Haloferax volcanii
            Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
            Halobacteriaceae; Haloferax.
REFERENCE   1  (bases 1 to 78)
  AUTHORS   Gupta,R.
  TITLE     Structural characterization of the transfer ribonucleic acids from
            Halobacterium volcanii and other archaebacteria
  JOURNAL   Unpublished (1981)
REFERENCE   2  (bases 1 to 78)
  AUTHORS   Gupta,R.
  TITLE     Halobacterium volcanii tRNAs. Identification of 41 tRNAs covering
            all amino acids, and the sequences of 33 class I tRNAs
  JOURNAL   J. Biol. Chem. 259 (15), 9461-9471 (1984)
  MEDLINE   84264593
   PUBMED   6746655
COMMENT     Original source text: Halobacterium volcanii, strain DS2 (NCMB
            2012; ATCC 29605) tRNA.
            A total of 41 tRNAs, at least one for each AA, were identified. The
            sequences of the 33 class I tRNAs, representing 18 AAs, are
            presented in [Thesis (1981) University of Illinois, Urbana]. As in
            eukaryotes, only Leu and Ser tRNAs are
            class II tRNAs (large extra arm).
            The archaebacterial tRNAs follow general tRNA patterns, but have
            certain characteristics so far not reported for other tRNAs: all
            have 'cm' at position 55; 'm1i' at position 56; 'm22g' at position
            10; 'm1f' at position 53; and possibly 'x' at position 15. Only
            archaebacteria modify the residue at position 15.
            The initiator tRNA is unique in that it has a 5'-phosphorylated
            end.
            [Thesis (1981) University of Illinois, Urbana] Contributed on tape
            April 1983 by M.Sprinzl & D.H.Gauss; from
            their entry 1315 in Nucleic Acids Res. 11, r1-r54 (1983).
FEATURES             Location/Qualifiers
     source          1. .78
                     /organism="Haloferax volcanii"
                     /mol_type="tRNA"
                     /db_xref="taxon:2246"
     tRNA            1. .78
                     /product="tRNA-Met"
                     /note="codon recognized: AUG; Met-tRNA-i (NAR: 1315)"
     modified_base   13
                     /mod_base=p
     modified_base   15
                     /mod_base=x
     modified_base   56
                     /mod_base=m1f
     modified_base   57
                     /mod_base=p
     modified_base   58
                     /mod_base=cm
     modified_base   59
                     /mod_base=m1i
ORIGIN      5' end of mature tRNA.

  Query Match             24.2%;  Score 23.2;  DB 1;  Length 78;
  Best Local Similarity   58.3%;  Pred. No. 4.4e+03;
  Matches   21;  Conservative    7;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         50 AUUCCGGAACGCUCAUAACCCAGAGGUCGAUAGUAC 85
              |::|||    ||:||:||||| ||| :|| :||: |
Db         23 ATTCCGCCGGGCTCATAACCCGGAGATCGGTAGTTC 58


RESULT 3
HCMET
LOCUS       HCMET                      78 bp    DNA     linear   BCT 11-JUN-2003
DEFINITION  Halobacterium cutirubrum transfer RNA-Met (CAU).
ACCESSION   X03199
VERSION     X03199.1  GI:43447
KEYWORDS    transfer RNA; transfer RNA-Met.
SOURCE      Halobacterium salinarum
  ORGANISM  Halobacterium salinarum
            Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
            Halobacteriaceae; Halobacterium.
REFERENCE   1  (bases 1 to 78)
  AUTHORS   Nicoghosian,K., Gu,X.R. and Cedergren,R.
  TITLE     Halobacterium cutirubrum tRNA sequences
  JOURNAL   FEBS Lett. 193, 255-260 (1985)
COMMENT     Data kindly reviewed (26-MAR-1986) by K. Nicoghosian.
FEATURES             Location/Qualifiers
     source          1. .78
                     /organism="Halobacterium salinarum"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:2242"
     tRNA            1. .78
                     /product="tRNA-Met"
     modified_base   13
                     /note="pseudouridine"
                     /mod_base=p
     modified_base   15
                     /note="unknown modified G"
                     /mod_base=OTHER
     modified_base   56
                     /note="1-methylpseudouridine"
                     /mod_base=m1f
     modified_base   57
                     /note="pseudouridine"
                     /mod_base=p
     modified_base   58
                     /note="2'O-methylcytidine"
                     /mod_base=OTHER
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     modified_base   59
                     /note="1-methylinosine"
                     /mod_base=mli
ORIGIN

  Query Match             24.2%;  Score 23.2;  DB 1;  Length 78;
  Best Local Similarity   58.3%;  Pred. No. 4.4e+03;
  Matches   21;  Conservative    7;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          50 AUUCCGGAACGCUCAUAACCCAGAGGUCGAUAGUAC 85
               |::|||    ||:||:||||| ||| :|| :||: |
Db          23 ATTCCGCCGGGCTCATAACCCGGAGATCGGTAGTTC 58


RESULT 4
AY006113/c
LOCUS       AY006113                 91 bp    mRNA    linear   PRI 26-SEP-2000
DEFINITION  Homo sapiens clone pbvb203 T cell receptor beta chain mRNA, partial
            cds.
ACCESSION   AY006113
VERSION     AY006113.1  GI:10304544
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 91)
  AUTHORS   Slachta,C.A., Jeevanandam,V., Goldman,B., Lin,W.L. and
            Platsoucas,C.D.
  TITLE     Coronary arteries from human cardiac allografts with chronic
            rejection contain oligoclonal T cells: persistence of identical
            clonally expanded TCR transcripts from the early
            post-transplantation period (endomyocardial biopsies) to chronic
            rejection (coronary arteries)
  JOURNAL   J. Immunol. 165 (6), 3469-3483 (2000)
  MEDLINE   20432336
   PUBMED   10975868
REFERENCE   2  (bases 1 to 91)
  AUTHORS   Slachta,C.A., Jeevanandam,V., Goldman,B.I., Lin,W.L. and
            Platsoucas,C.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2000) Departmant of Microbiology and Immunology,
            Temple University School of Medicine, 3400 N. Broad Street,
            Philadelphia, PA 19140, USA
FEATURES             Location/Qualifiers
     source          1. .91
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="pbvb203"
                     /tissue_type="peripheral blood mononuclear cells"
                     /rearranged
                     /note="contains Vb2.1 Db2.1 Jb2.3"
     CDS             <1. .>91
                     /note="CDR3 region; consists of 3'V-beta, Db, and
                     5'J-beta"
                     /codon_start=1
                     /product="T cell receptor beta chain"
                     /protein_id="AAG15616.1"
                     /db_xref="GI:10304545"
                     /translation="DSSFYICSASFSEREDTDTQYFGPGTRLTV"
ORIGIN

  Query Match             24.2%;  Score 23.2;  DB 9;  Length 91;
  Best Local Similarity   45.6%;  Pred. No. 4.4e+03;
  Matches   31;  Conservative    9;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          20 GGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGA 79
               ||  |  |:|| |||:|    :| |: |||  :| | || ||:   |   |||| |: ||
Db          70 GGCCAAAATACTGCGTATCTGTGTCTTCCCGCTCGGAAAAGCTAGCACTGCAGATGTAGA 11

Qy          80 UAGUACUG 87
                 : |:|
Db          10 AGCTGCTG 3


RESULT 5
AB059449/c
LOCUS       AB059449                 99 bp    DNA     linear   BCT 25-APR-2001
DEFINITION  Uncultured bacterium gene for 16S rRNA, partial sequence,
            clone:B2_538-14(B14).
ACCESSION   AB059449
VERSION     AB059449.2  GI:13785490
KEYWORDS    .
SOURCE      uncultured bacterium
  ORGANISM  uncultured bacterium
            Bacteria; environmental samples.
REFERENCE   1  (sites)
  AUTHORS   Ueno,Y., Haruta,S., Ishii,M. and Igarashi,Y.
  TITLE     Changes in Product Formation and Bacterial Community on
            Carbohydrate Fermentation by Anaerobic Microflora -Effects of
            Dilution Rate in Continuous Flow Stirred Tank Reactor-
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 99)
  AUTHORS   Ueno,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-APR-2001) Yoshiyuki Ueno, Kajima Technical Research
            Institute, Bio-environment group; Tibitakyu, 2-19-1, Chofu-shi,
            Tokyo 182-0036, Japan (E-mail:yoshi-u@katri.kajima.co.jp,
            Tel:81-424-89-7066(ex.2945), Fax:81-424-89-2896)
COMMENT     On Apr 24, 2001 this sequence version replaced gi:13620946.
FEATURES             Location/Qualifiers
     source          1. .99
                     /organism="uncultured bacterium"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:77133"
                     /clone="B2_538-14(B14)"
                     /note="DGGE fragment of anaerobic microflora"
     rRNA            <1. .>99
                     /product="16S ribosomal RNA"
ORIGIN

  Query Match             23.8%;  Score 22.8;  DB 1;  Length 99;
  Best Local Similarity   50.0%;  Pred. No. 6e+03;
  Matches   25;  Conservative    8;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          28 UACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUC 77
               :|||| :  : |: | :||||| :| |  | | : | |||||  |||:|
Db          69 TACCGTCTCTTTCTTCGTCCCCAATCAGAGAAGTTTACAACCCGAAGGTC 20


RESULT 6
AB059200/c
LOCUS       AB059200                181 bp    DNA     linear   STS 19-MAR-2002
DEFINITION  Sus scrofa domestica genomic DNA, chromosome 7, 346D10R, sequence
            tagged site.
ACCESSION   AB059200
VERSION     AB059200.1  GI:19570733
KEYWORDS    STS.
SOURCE      Sus scrofa domestica (domestic pig)
  ORGANISM  Sus scrofa domestica
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1
  AUTHORS   Kiuchi,S., Inage,Y., Hiraiwa,H., Uenishi,H. and Yasue,H.
  TITLE     Assignment of 280 swine genomic inserts including 31
            microsatellites from BAC clones to the swine RH map (IMpRH map)
  JOURNAL   Mamm. Genome 13 (2), 80-88 (2002)
  MEDLINE   21886643
   PUBMED   11889555
REFERENCE   2  (bases 1 to 181)
  AUTHORS   Kiuchi,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-MAR-2001) Sachiko Kiuchi, National Institute of
            Agrobiological Sciences, Genome Research Group; 2 Ikenodai,
            Kukizaki-machi, Inashiki-gun, Ibaraki 305-0901, Japan
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           (E-mail:sachikok@affrc.go.jp, Tel:81-298-38-8664,
           Fax:81-298-38-8674)
FEATURES             Location/Qualifiers
     source          1. .181
                     /organism="Sus scrofa domestica"
                     /mol_type="genomic DNA"
                     /sub_species="domestica"
                     /db_xref="taxon:9825"
                     /chromosome="7"
                     /clone="346D10"
                     /clone_lib="Swine genomic BAC library, National Institute
                     of Agrobiological Resources, Ibaraki, Japan"
                     /note="synonym:Sus scrofa domesticus"
     STS             1. .181
                     /standard_name="346D10R"
     primer_bind     1. .20
                     /PCR_conditions="denaturation 30s at 95 degrees, annealing
                     30s at 57 degrees, extension 30s at 72 degrees, final
                     elongation 5min at 72 degrees, 40 cycles"
     primer_bind     complement(162. .181)
ORIGIN

  Query Match            22.9%;  Score 22;  DB 11;  Length 181;
  Best Local Similarity  55.6%;  Pred. No. 1.1e+04;
  Matches   30;  Conservative    4;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCC 54
              ||  | | || |||||| :|||||  | || |  :|| ||:|  :  | |  ||
Db         94 GGTGGTGGGGGAGAGGGCTGGGGAGCAGACTGAATAAGGCTGGATGTCAAAGCC 41


RESULT 7
AU046875/c
LOCUS       AU046875               187 bp    DNA     linear   STS 22-APR-1999
DEFINITION  Rattus norvegicus, OTSUKA clone, 085b01, microsatellite sequence,
            sequence tagged site.
ACCESSION   AU046875
VERSION     AU046875.1  GI:4631510
KEYWORDS    STS.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (sites)
  AUTHORS   Watanabe,T.K., Hishigaki,H., Okuno,S., Mizoguchi,A., Oga,K.,
            Tsuji,A., Ono,T., Yamasaki,Y., Kanemoto,N., Takahashi,E., Irie,Y.,
            Nakamura,Y., Takagi,Y. and Tanigami,A.
  TITLE     The large-scale mapping of rat microsatellite markers
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 187)
  AUTHORS   Watanabe,T.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-DEC-1998) Takeshi K Watanabe, Otsuka GEN Research
            Institute, Otsuka Pharmaceutical Co., Ltd; 463-10, Kagasuno,
            Kawauchi-cho, Tokushima, Tokushima 771-0192, Japan
            (E-mail:watanabe@otsuka.gr.jp, Tel:+81-886-65-2888,
            Fax:+81-886-37-1035)
FEATURES             Location/Qualifiers
     source          1. .187
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /strain="Brown Norway"
                     /db_xref="taxon:10116"
                     /clone="085b01"
                     /cell_type="hepatocyte"
                     /tissue_type="liver"
                     /note="085b01F=5'-TCTCTCTCCCTCCCTCCCT-3',
                     085b01R=5'-AGACTTTGTACACACACACGCA-3'"
ORIGIN

  Query Match            22.9%;  Score 22;  DB 11;  Length 187;
  Best Local Similarity  51.9%;  Pred. No. 1.1e+04;
  Matches   28;  Conservative    6;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCCAUUCC 54
              |||||  |||| || | ||  | || :|: ||    ||  |: ||:||   :: |
Db         62 GGGAGGGAGGGAGGGAGAGAGAGATTATTCCATAAAAGTCTCCCTCCTGCTTAC 9


RESULT 8
AR141692
LOCUS       AR141692               108 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 3 from patent US 6146886.
ACCESSION   AR141692
VERSION     AR141692.1  GI:15101208
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 108)
  AUTHORS   Thompson,J.D.
  TITLE     RNA polymerase III-based expression of therapeutic RNAs
  JOURNAL   Patent: US 6146886-A 3 14-NOV-2000;
FEATURES             Location/Qualifiers
     source          1. .108
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            22.7%;  Score 21.8;  DB 6;  Length 108;
  Best Local Similarity  52.3%;  Pred. No. 1.3e+04;
  Matches   34;  Conservative    4;  Mismatches   27;  Indels    0;  Gaps    0;

Qy         29 ACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGAUAGUACUGG 88
              || ||  | :|  ||  |   |    |    || ||:||||||||||:|||: |  |
Db          7 ACAGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCCATAACCCAGAGGTCGATGGATCGAA 66

Qy         89 AUCCC 93
              | |||  .
Db         67 ACCCC 71


RESULT 9
AX638750
LOCUS       AX638750               108 bp    RNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 5889 from Patent EP1260586.
ACCESSION   AX638750
VERSION     AX638750.1  GI:28474364
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
  TITLE     Method and reagent for inhibiting the expression of disease related
            genes
  JOURNAL   Patent: EP 1260586-A 5889 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .108
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                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32644"
ORIGIN

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  Best Local Similarity  52.3%;  Pred. No. 1.3e+04;
  Matches   34;  Conservative    4;  Mismatches   27;  Indels    0;  Gaps    0;

Qy         29 ACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGAUAGUACUGG 88
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Db          7 ACAGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCCATAACCCAGAGGTCGATGGATCGAA 66

Qy         89 AUCCC 93
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Db         67 ACCCC 71
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RESULT 10
AR141696
LOCUS AR141696 109 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 7 from patent US 6146886.
ACCESSION AR141696
VERSION AR141696.1 GI:15101212
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 109)
AUTHORS Thompson,J.D.
TITLE RNA polymerase III-based expression of therapeutic RNAs
JOURNAL Patent: US 6146886-A 7 14-NOV-2000;
FEATURES Location/Qualifiers
source 1. .109
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

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  Query Match             22.7%;  Score 21.8;  DB 6;  Length 109;
  Best Local Similarity   52.3%;  Pred. No. 1.3e+04;
  Matches   34;  Conservative    4;  Mismatches   27;  Indels    0;  Gaps    0;

Qy         29 ACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGAUAGUACUGG 88
              || ||  | :|  ||  |   |    |    || ||:|||||||||||:|||: |  |
Db          7 ACAGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCCATAACCCAGAGGTCGATGGATCGAA 66

Qy         89 AUCCC 93
              | |||
Db         67 ACCCC 71
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RESULT 11
AX638754
LOCUS AX638754 109 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 5893 from Patent EP1260586.
ACCESSION AX638754
VERSION AX638754.1 GI:28474368
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A., Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J., Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related genes
JOURNAL Patent: EP 1260586-A 5893 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES Location/Qualifiers
source 1. .109
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ORIGIN

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  Best Local Similarity   52.3%;  Pred. No. 1.3e+04;
  Matches   34;  Conservative    4;  Mismatches   27;  Indels    0;  Gaps    0;

Qy         29 ACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGAUAGUACUGG 88
              || ||  | :|  ||  |   |    |    || ||:|||||||||||:|||: |  |
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Db          7 ACAGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCCATAACCCAGAGGTCGATGGATCGAA 66

Qy         89 AUCCC 93
              | |||
Db         67 ACCCC 71
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RESULT 12
AR141694
LOCUS AR141694 133 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 5 from patent US 6146886.
ACCESSION AR141694
VERSION AR141694.1 GI:15101210
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 133)
AUTHORS Thompson,J.D.
TITLE RNA polymerase III-based expression of therapeutic RNAs
JOURNAL Patent: US 6146886-A 5 14-NOV-2000;
FEATURES Location/Qualifiers
source 1. .133
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

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  Query Match             22.7%;  Score 21.8;  DB 6;  Length 133;
  Best Local Similarity   52.3%;  Pred. No. 1.3e+04;
  Matches   34;  Conservative    4;  Mismatches   27;  Indels    0;  Gaps    0;

Qy         29 ACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGAUAGUACUGG 88
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Db          7 ACAGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCCATAACCCAGAGGTCGATGGATCGAA 66

Qy         89 AUCCC 93
              | |||
Db         67 ACCCC 71
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RESULT 13
AR141698
LOCUS AR141698 133 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 9 from patent US 6146886.
ACCESSION AR141698
VERSION AR141698.1 GI:15101214
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 133)
AUTHORS Thompson,J.D.
TITLE RNA polymerase III-based expression of therapeutic RNAs
JOURNAL Patent: US 6146886-A 9 14-NOV-2000;
FEATURES Location/Qualifiers
source 1. .133
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

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  Best Local Similarity   52.3%;  Pred. No. 1.3e+04;
  Matches   34;  Conservative    4;  Mismatches   27;  Indels    0;  Gaps    0;

Qy         29 ACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGAUAGUACUGG 88
              || ||  | :|  ||  |   |    |    || ||:|||||||||||:|||: |  |
Db          7 ACAGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCCATAACCCAGAGGTCGATGGATCGAA 66

Qy         89 AUCCC 93
              | |||
Db         67 ACCCC 71
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RESULT 14
AX638752
LOCUS       AX638752                133 bp    RNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 5891 from Patent EP1260586.
ACCESSION   AX638752
VERSION     AX638752.1  GI:28474366
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
  TITLE     Method and reagent for inhibiting the expression of disease related
            genes
  JOURNAL   Patent: EP 1260586-A 5891 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .133
                     /organism="unidentified"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match            22.7%;  Score 21.8;  DB 6;  Length 133;
  Best Local Similarity  52.3%;  Pred. No. 1.3e+04;
  Matches   34;  Conservative    4;  Mismatches   27;  Indels    0;  Gaps    0;

Qy         29 ACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGAUAGUACUGG 88
              || ||  | :|  ||  |   |    |    || ||:||||||||||:|||: |  |
Db          7 ACAGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCCATAACCCAGAGGTCGATGGATCGAA 66

Qy         89 AUCCC 93
              | |||
Db         67 ACCCC 71


RESULT 15
AX638756
LOCUS       AX638756                133 bp    RNA     linear   PAT 24-FEB-2003
DEFINITION  Sequence 5895 from Patent EP1260586.
ACCESSION   AX638756
VERSION     AX638756.1  GI:28474370
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
  TITLE     Method and reagent for inhibiting the expression of disease related
            genes
  JOURNAL   Patent: EP 1260586-A 5895 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .133
                     /organism="unidentified"
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                     /db_xref="taxon:32644"
ORIGIN

  Query Match            22.7%;  Score 21.8;  DB 6;  Length 133;
  Best Local Similarity  52.3%;  Pred. No. 1.3e+04;
  Matches   34;  Conservative    4;  Mismatches   27;  Indels    0;  Gaps    0;

Qy         29 ACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGAUAGUACUGG 88
              || ||  | :|  ||  |   |    |    || ||:||||||||||:|||: |  |
Db          7 ACAGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCCATAACCCAGAGGTCGATGGATCGAA 66

Qy         89 AUCCC 93
              | |||
Db         67 ACCCC 71


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GenCore version 5.1.6

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Title: US-09-963-827B-3
Perfect score: 96
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 3774412

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	96	100.0	96	6	ABN88490	Abn88490 Coagulati
2	62	64.6	94	6	ABN88506	Abn88506 Coagulati
3	60.8	63.3	96	6	ABN88504	Abn88504 Coagulati
4	60	62.5	95	6	ABN88509	Abn88509 Coagulati
5	59.2	61.7	96	6	ABN88489	Abn88489 Coagulati
6	58.4	60.8	95	6	ABN88499	Abn88499 Coagulati
7	58.4	60.8	95	6	ABN88491	Abn88491 Coagulati
8	56	58.3	96	6	ABN88497	Abn88497 Coagulati
9	56	58.3	96	6	ABN88500	Abn88500 Coagulati
10	55	57.3	96	6	ABN88502	Abn88502 Coagulati
11	54.4	56.7	96	6	ABN88527	Abn88527 Coagulati
12	52.8	55.0	96	6	ABN88521	Abn88521 Coagulati
13	51.2	53.3	96	6	ABN88510	Abn88510 Coagulati
14	50.8	52.9	96	6	ABN88498	Abn88498 Coagulati
15	49.6	51.7	96	6	ABN88501	Abn88501 Coagulati
16	49.6	51.7	96	6	ABN88496	Abn88496 Coagulati
17	49.6	51.7	96	6	ABN88503	Abn88503 Coagulati
18	49.6	51.7	96	6	ABN88493	Abn88493 Coagulati
19	49.6	51.7	96	6	ABN88531	Abn88531 Coagulati
20	49.6	51.7	96	6	ABN88528	Abn88528 Coagulati
21	49.6	51.7	96	6	ABN88526	Abn88526 Coagulati
22	48	50.0	96	6	ABN88529	Abn88529 Coagulati
23	48	50.0	96	6	ABN88508	Abn88508 Coagulati
24	48	50.0	96	6	ABN88530	Abn88530 Coagulati
25	47.2	49.2	92	6	ABN88559	Abn88559 Coagulati
26	47.2	49.2	95	6	ABN88507	Abn88507 Coagulati
27	47.2	49.2	95	6	ABN88515	Abn88515 Coagulati
28	46.6	48.5	97	6	ABN88511	Abn88511 Coagulati
29	46.4	48.3	96	6	ABN88533	Abn88533 Coagulati
30	46.4	48.3	96	6	ABN88492	Abn88492 Coagulati
31	46.4	48.3	96	6	ABN88532	Abn88532 Coagulati
32	46.4	48.3	96	6	ABN88534	Abn88534 Coagulati
33	46.4	48.3	96	6	ABN88505	Abn88505 Coagulati
34	46.2	48.1	99	6	ABN88518	Abn88518 Coagulati
35	45	46.9	97	6	ABN88523	Abn88523 Coagulati
36	45	46.9	97	6	ABN88514	Abn88514 Coagulati
37	44.8	46.7	96	6	ABN88494	Abn88494 Coagulati
38	43.4	45.2	92	6	ABN88512	Abn88512 Coagulati
39	43.4	45.2	97	6	ABN88519	Abn88519 Coagulati
40	43.2	45.0	96	6	ABN88488	Abn88488 Coagulati
41	41.8	43.5	97	6	ABN88516	Abn88516 Coagulati
42	41.8	43.5	97	6	ABN88513	Abn88513 Coagulati
43	40.4	42.1	100	6	ABN88520	Abn88520 Coagulati
44	40.2	41.9	97	6	ABN88524	Abn88524 Coagulati
45	40	41.7	40	7	ABZ21242	Abz21242 FIXa apta

ALIGNMENTS

RESULT 1
ABN88490
ID ABN88490 standard; RNA; 96 BP.
XX
AC ABN88490;
XX
DT 19-AUG-2002 (first entry)
XX
DE Coagulation factor IXa binding/inhibiting RNA aptamer SEQ ID NO:3.
XX
KW RNA aptamer; identification; coagulation factor; angiopoietin; thrombin;
KW E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant;
KW cell proliferation; intimal hyperplasia; angiogenesis;
KW bypass graft surgery; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200226932-A2.
XX
PD 04-APR-2002.
XX
PF 26-SEP-2001; 2001WO-US030004.
XX
PR 26-SEP-2000; 2000US-0235654P.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Sullenger BA, Rusconi CP;
XX
DR WPI; 2002-479560/51.
XX
PT Novel RNA aptamers that selectively bind coagulation pathway factors, E2F
PT family members, Ang1 or Ang2, useful for modulating coagulation pathway
PT factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.
XX
PS Claim 13; Fig 1A; 216pp; English.
XX
CC The present invention describes RNA aptamers (I,II,III) that selectively
CC bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c)
CC angiopoietin-1 (Ang1) or Ang2, respectively, where (I), (II), (III) have
CC a dissociation constant for the coagulation pathway factor, an E2F family
CC member, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) have
CC cardiant and cytostatic activities. (I) are useful for modulating the
CC biological activity of a coagulation pathway factor which involves
CC administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that

CC the biological activity of the coagulation pathway factor in the warm-
CC blooded vertebrate is modulated. (I) are also useful for treating
CC cardiovascular diseases in the mammal. (II) are useful for modulating E2F
CC activity in a warm-blooded vertebrate. (III) are useful for modulating
CC Ang1 or Ang2 activity in a warm-blooded vertebrate. (I) are potent
CC anticoagulants and significantly delay the clotting time of normal human
CC plasma or the activation of platelets in response to thrombin. (II) are
CC useful for inhibiting cell proliferation in a number of conditions e.g.,
CC intimal hyperplasia following bypass graft surgery. (III) are useful for
CC modulating angiogenesis. The RNA aptamers are also useful for diagnostic,
CC research and therapeutic context. The aptamers are useful as diagnostic
CC reagents to detect the presence or absence of target substances to which
CC they specifically bind, and for identifying substances to which they
CC specifically bind, for isolating and purifying substances to which they
CC bind, and as a separation reagent for retrieving the targets to which
CC they specifically bind. ABN88488 to ABN88713 and ABB81231 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 96 BP; 24 A; 27 C; 29 G; 0 T; 16 U; 0 Other;

Query Match 100.0%; Score 96; DB 6; Length 96;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60

Qy 61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
Db 61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96

RESULT 2
ABN88506
ID ABN88506 standard; RNA; 94 BP.
XX
AC ABN88506;
XX
DT 19-AUG-2002 (first entry)
XX
DE Coagulation factor IXa binding/inhibiting RNA aptamer SEQ ID NO:19.
XX
KW RNA aptamer; identification; coagulation factor; angiopoietin; thrombin;
KW E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant;
KW cell proliferation; intimal hyperplasia; angiogenesis;
KW bypass graft surgery; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200226932-A2.
XX
PD 04-APR-2002.
XX
PF 26-SEP-2001; 2001WO-US030004.
XX
PR 26-SEP-2000; 2000US-0235654P.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Sullenger BA, Rusconi CP;
XX
DR WPI; 2002-479560/51.
XX
PT Novel RNA aptamers that selectively bind coagulation pathway factors, E2F
PT family members, Ang1 or Ang2, useful for modulating coagulation pathway
PT factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.
XX
PS Claim 13; Fig 1B; 216pp; English.
XX
CC The present invention describes RNA aptamers (I,II,III) that selectively
CC bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c)
CC angiopoietin-1 (Ang1) or Ang2, respectively, where (I), (II), (III) have
CC a dissociation constant for the coagulation pathway factor, an E2F family
CC member, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) have
CC cardiant and cytostatic activities. (I) are useful for modulating the
CC biological activity of a coagulation pathway factor which involves
CC administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that
CC the biological activity of the coagulation pathway factor in the warm-
CC blooded vertebrate is modulated. (I) are also useful for treating
CC cardiovascular diseases in the mammal. (II) are useful for modulating E2F
CC activity in a warm-blooded vertebrate. (III) are useful for modulating
CC Ang1 or Ang2 activity in a warm-blooded vertebrate. (I) are potent
CC anticoagulants and significantly delay the clotting time of normal human
CC plasma or the activation of platelets in response to thrombin. (II) are
CC useful for inhibiting cell proliferation in a number of conditions e.g.,
CC intimal hyperplasia following bypass graft surgery. (III) are useful for
CC modulating angiogenesis. The RNA aptamers are also useful for diagnostic,
CC research and therapeutic context. The aptamers are useful as diagnostic
CC reagents to detect the presence or absence of target substances to which
CC they specifically bind, and for identifying substances to which they
CC specifically bind, for isolating and purifying substances to which they
CC bind, and as a separation reagent for retrieving the targets to which
CC they specifically bind. ABN88488 to ABN88713 and ABB81231 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 94 BP; 29 A; 22 C; 28 G; 0 T; 15 U; 0 Other;

Query Match 64.6%; Score 62; DB 6; Length 94;
Best Local Similarity 78.7%; Pred. No. 7.4e-13;
Matches 74; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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Db 1 GGGAGAGAGGAAGAGGGAUGGGGACCAUAACUCUAACGGGUGAAUCCCGCAUCUCGACAA 60

Qy 61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCC 94
Db 61 UACAUAACCCAGAGGUCGAUAGUACUGGAUCCCC 94

RESULT 3
ABN88504
ID ABN88504 standard; RNA; 96 BP.
XX
AC ABN88504;
XX
DT 19-AUG-2002 (first entry)
XX
DE Coagulation factor IXa binding/inhibiting RNA aptamer SEQ ID NO:17.
XX
KW RNA aptamer; identification; coagulation factor; angiopoietin; thrombin;
KW E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant;
KW cell proliferation; intimal hyperplasia; angiogenesis;
KW bypass graft surgery; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200226932-A2.
XX
PD 04-APR-2002.
XX
PF 26-SEP-2001; 2001WO-US030004.
XX
PR 26-SEP-2000; 2000US-0235654P.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Sullenger BA, Rusconi CP;
XX
DR WPI; 2002-479560/51.
XX
PT Novel RNA aptamers that selectively bind coagulation pathway factors, E2F
PT family members, Ang1 or Ang2, useful for modulating coagulation pathway

PT factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.
XX
PS Claim 13; Fig 1B; 216pp; English.
XX
CC The present invention describes RNA aptamers (I,II,III) that selectively
CC bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c)
CC angiopoietin-1 (Ang1) or Ang2, respectively, where (I), (II), (III) have
CC a dissociation constant for the coagulation pathway factor, an E2F family
CC member, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) have
CC cardiant and cytostatic activities. (I) are useful for modulating the
CC biological activity of a coagulation pathway factor which involves
CC administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that
CC the biological activity of the coagulation pathway factor in the warm-
CC blooded vertebrate is modulated. (I) are also useful for treating
CC cardiovascular diseases in the mammal. (II) are useful for modulating E2F
CC activity in a warm-blooded vertebrate. (III) are useful for modulating
CC Ang1 or Ang2 activity in a warm-blooded vertebrate. (I) are potent
CC anticoagulants and significantly delay the clotting time of normal human
CC plasma or the activation of platelets in response to thrombin. (II) are
CC useful for inhibiting cell proliferation in a number of conditions e.g.,
CC intimal hyperplasia following bypass graft surgery. (III) are useful for
CC modulating angiogenesis. The RNA aptamers are also useful for diagnostic,
CC research and therapeutic context. The aptamers are useful as diagnostic
CC reagents to detect the presence or absence of target substances to which
CC they specifically bind, and for identifying substances to which they
CC specifically bind, for isolating and purifying substances to which they
CC bind, and as a separation reagent for retrieving the targets to which
CC they specifically bind. ABN88488 to ABN88713 and ABB81231 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 96 BP; 28 A; 25 C; 28 G; 0 T; 15 U; 0 Other;

Query Match 63.3%; Score 60.8; DB 6; Length 96;
Best Local Similarity 77.1%; Pred. No. 2.1e-12;
Matches 74; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

```
Qy          1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
              ||||||||||||||||||||||||||||||||   |  |      |||    ||  |
Db          1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGGCAAUCGUGCAUCCCCUGGACCUAACAA 60

Qy         61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
              ||||||||||||||||||||||||||||||||||||
Db         61 UACAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
```

RESULT 4
ABN88509
ID ABN88509 standard; RNA; 95 BP.
XX
AC ABN88509;
XX
DT 19-AUG-2002 (first entry)
XX
DE Coagulation factor IXa binding/inhibiting RNA aptamer SEQ ID NO:22.
XX
KW RNA aptamer; identification; coagulation factor; angiopoietin; thrombin;
KW E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant;
KW cell proliferation; intimal hyperplasia; angiogenesis;
KW bypass graft surgery; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200226932-A2.
XX
PD 04-APR-2002.
XX
PF 26-SEP-2001; 2001WO-US030004.
XX
PR 26-SEP-2000; 2000US-0235654P.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Sullenger BA, Rusconi CP;
XX
DR WPI; 2002-479560/51.
XX
PT Novel RNA aptamers that selectively bind coagulation pathway factors, E2F
PT family members, Ang1 or Ang2, useful for modulating coagulation pathway
PT factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.
XX
PS Claim 13; Fig 1B; 216pp; English.
XX
CC The present invention describes RNA aptamers (I,II,III) that selectively
CC bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c)
CC angiopoietin-1 (Ang1) or Ang2, respectively, where (I), (II), (III) have
CC a dissociation constant for the coagulation pathway factor, an E2F family
CC member, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) have
CC cardiant and cytostatic activities. (I) are useful for modulating the
CC biological activity of a coagulation pathway factor which involves
CC administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that
CC the biological activity of the coagulation pathway factor in the warm-
CC blooded vertebrate is modulated. (I) are also useful for treating
CC cardiovascular diseases in the mammal. (II) are useful for modulating E2F
CC activity in a warm-blooded vertebrate. (III) are useful for modulating
CC Ang1 or Ang2 activity in a warm-blooded vertebrate. (I) are potent
CC anticoagulants and significantly delay the clotting time of normal human
CC plasma or the activation of platelets in response to thrombin. (II) are
CC useful for inhibiting cell proliferation in a number of conditions e.g.,
CC intimal hyperplasia following bypass graft surgery. (III) are useful for
CC modulating angiogenesis. The RNA aptamers are also useful for diagnostic,
CC research and therapeutic context. The aptamers are useful as diagnostic
CC reagents to detect the presence or absence of target substances to which
CC they specifically bind, and for identifying substances to which they
CC specifically bind, for isolating and purifying substances to which they
CC bind, and as a separation reagent for retrieving the targets to which
CC they specifically bind. ABN88488 to ABN88713 and ABB81231 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 95 BP; 25 A; 27 C; 28 G; 0 T; 15 U; 0 Other;

Query Match 62.5%; Score 60; DB 6; Length 95;
Best Local Similarity 83.3%; Pred. No. 4e-12;
Matches 80; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

```
Qy          1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
              ||||||||||||||||||||  | ||| |||  | ||||| || || | ||| ||
Db          1 GGGAGAGAGGAAGAGGGAUGGGCGCCAUA-CGCACAUUGCUGCAUCGCCUUCCCGUAAGA 59

Qy         61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
              ||||||||||||||||||||||||||||||||||||
Db         60 ACCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 95
```

RESULT 5
ABN88489
ID ABN88489 standard; RNA; 96 BP.
XX
AC ABN88489;
XX
DT 19-AUG-2002 (first entry)
XX
DE Coagulation factor IXa binding/inhibiting RNA aptamer SEQ ID NO:2.
XX
KW RNA aptamer; identification; coagulation factor; angiopoietin; thrombin;
KW E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant;
KW cell proliferation; intimal hyperplasia; angiogenesis;
KW bypass graft surgery; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200226932-A2.
XX
PD 04-APR-2002.
XX

PF 26-SEP-2001; 2001WO-US030004.
XX
PR 26-SEP-2000; 2000US-0235654P.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Sullenger BA, Rusconi CP;
XX
DR WPI; 2002-479560/51.
XX
PT Novel RNA aptamers that selectively bind coagulation pathway factors, E2F
PT family members, Ang1 or Ang2, useful for modulating coagulation pathway
PT factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.
XX
PS Claim 13; Fig 1A; 216pp; English.
XX
CC The present invention describes RNA aptamers (I,II,III) that selectively
CC bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c)
CC angiopoietin-1 (Ang1) or Ang2, respectively, where (I), (II), (III) have
CC a dissociation constant for the coagulation pathway factor, an E2F family
CC member, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) have
CC cardiant and cytostatic activities. (I) are useful for modulating the
CC biological activity of a coagulation pathway factor which involves
CC administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that
CC the biological activity of the coagulation pathway factor in the warm-
CC blooded vertebrate is modulated. (I) are also useful for treating
CC cardiovascular diseases in the mammal. (II) are useful for modulating E2F
CC activity in a warm-blooded vertebrate. (III) are useful for modulating
CC Ang1 or Ang2 activity in a warm-blooded vertebrate. (I) are potent
CC anticoagulants and significantly delay the clotting time of normal human
CC plasma or the activation of platelets in response to thrombin. (II) are
CC useful for inhibiting cell proliferation in a number of conditions e.g.,
CC intimal hyperplasia following bypass graft surgery. (III) are useful for
CC modulating angiogenesis. The RNA aptamers are also useful for diagnostic,
CC research and therapeutic context. The aptamers are useful as diagnostic
CC reagents to detect the presence or absence of target substances to which
CC they specifically bind, and for identifying substances to which they
CC specifically bind, for isolating and purifying substances to which they
CC bind, and as a separation reagent for retrieving the targets to which
CC they specifically bind. ABN88488 to ABN88713 and ABB81231 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 96 BP; 30 A; 23 C; 26 G; 0 T; 17 U; 0 Other;

Query Match 61.7%; Score 59.2; DB 6; Length 96;
Best Local Similarity 76.0%; Pred. No. 7.9e-12;
Matches 73; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
Db 1 GGGAGAGAGGAAGAGGGAUGGGCUAUAUACACGCUGGUGAUCCCAUCUCAAUUGAAACAA 60

Qy 61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
Db 61 CACAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96

RESULT 6
ABN88499
ID ABN88499 standard; RNA; 95 BP.
XX
AC ABN88499;
XX
DT 19-AUG-2002 (first entry)
XX
DE Coagulation factor IXa binding/inhibiting RNA aptamer SEQ ID NO:12.
XX
KW RNA aptamer; identification; coagulation factor; angiopoietin; thrombin;
KW E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant;
KW cell proliferation; intimal hyperplasia; angiogenesis;
KW bypass graft surgery; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200226932-A2.
XX
PD 04-APR-2002.
XX
PF 26-SEP-2001; 2001WO-US030004.
XX
PR 26-SEP-2000; 2000US-0235654P.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Sullenger BA, Rusconi CP;
XX
DR WPI; 2002-479560/51.
XX
PT Novel RNA aptamers that selectively bind coagulation pathway factors, E2F
PT family members, Ang1 or Ang2, useful for modulating coagulation pathway
PT factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.
XX
PS Claim 13; Fig 1A; 216pp; English.
XX
CC The present invention describes RNA aptamers (I,II,III) that selectively
CC bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c)
CC angiopoietin-1 (Ang1) or Ang2, respectively, where (I), (II), (III) have
CC a dissociation constant for the coagulation pathway factor, an E2F family
CC member, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) have
CC cardiant and cytostatic activities. (I) are useful for modulating the
CC biological activity of a coagulation pathway factor which involves
CC administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that
CC the biological activity of the coagulation pathway factor in the warm-
CC blooded vertebrate is modulated. (I) are also useful for treating
CC cardiovascular diseases in the mammal. (II) are useful for modulating E2F
CC activity in a warm-blooded vertebrate. (III) are useful for modulating
CC Ang1 or Ang2 activity in a warm-blooded vertebrate. (I) are potent
CC anticoagulants and significantly delay the clotting time of normal human
CC plasma or the activation of platelets in response to thrombin. (II) are
CC useful for inhibiting cell proliferation in a number of conditions e.g.,
CC intimal hyperplasia following bypass graft surgery. (III) are useful for
CC modulating angiogenesis. The RNA aptamers are also useful for diagnostic,
CC research and therapeutic context. The aptamers are useful as diagnostic
CC reagents to detect the presence or absence of target substances to which
CC they specifically bind, and for identifying substances to which they
CC specifically bind, for isolating and purifying substances to which they
CC bind, and as a separation reagent for retrieving the targets to which
CC they specifically bind. ABN88488 to ABN88713 and ABB81231 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 95 BP; 25 A; 26 C; 29 G; 0 T; 15 U; 0 Other;

Query Match 60.8%; Score 58.4; DB 6; Length 95;
Best Local Similarity 82.3%; Pred. No. 1.6e-11;
Matches 79; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

Qy 1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
Db 1 GGGAGAGAGGAAGAGGGAUGGGGACUAUA-CGUGAACGACUGCAUCCACUUCCCCGCCAU 59

Qy 61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
Db 60 GGCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 95

RESULT 7
ABN88491
ID ABN88491 standard; RNA; 95 BP.
XX
AC ABN88491;
XX
DT 19-AUG-2002 (first entry)
XX
DE Coagulation factor IXa binding/inhibiting RNA aptamer SEQ ID NO:4.
XX

KW RNA aptamer; identification; coagulation factor; angiopoietin; thrombin;
KW E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant;
KW cell proliferation; intimal hyperplasia; angiogenesis;
KW bypass graft surgery; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200226932-A2.
XX
PD 04-APR-2002.
XX
PF 26-SEP-2001; 2001WO-US030004.
XX
PR 26-SEP-2000; 2000US-0235654P.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Sullenger BA, Rusconi CP;
XX
DR WPI; 2002-479560/51.
XX
PT Novel RNA aptamers that selectively bind coagulation pathway factors, E2F
PT family members, Ang1 or Ang2, useful for modulating coagulation pathway
PT factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.
XX
PS Claim 13; Fig 1A; 216pp; English.
XX
CC The present invention describes RNA aptamers (I,II,III) that selectively
CC bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c)
CC angiopoietin-1 (Ang1) or Ang2, respectively, where (I), (II), (III) have
CC a dissociation constant for the coagulation pathway factor, an E2F family
CC member, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) have
CC cardiant and cytostatic activities. (I) are useful for modulating the
CC biological activity of a coagulation pathway factor which involves
CC administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that
CC the biological activity of the coagulation pathway factor in the warm-
CC blooded vertebrate is modulated. (I) are also useful for treating
CC cardiovascular diseases in the mammal. (II) are useful for modulating E2F
CC activity in a warm-blooded vertebrate. (III) are useful for modulating
CC Ang1 or Ang2 activity in a warm-blooded vertebrate. (I) are potent
CC anticoagulants and significantly delay the clotting time of normal human
CC plasma or the activation of platelets in response to thrombin. (II) are
CC useful for inhibiting cell proliferation in a number of conditions e.g.,
CC intimal hyperplasia following bypass graft surgery. (III) are useful for
CC modulating angiogenesis. The RNA aptamers are also useful for diagnostic,
CC research and therapeutic context. The aptamers are useful as diagnostic
CC reagents to detect the presence or absence of target substances to which
CC they specifically bind, and for identifying substances to which they
CC specifically bind, for isolating and purifying substances to which they
CC bind, and as a separation reagent for retrieving the targets to which
CC they specifically bind. ABN88488 to ABN88713 and ABB81231 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 95 BP; 24 A; 25 C; 29 G; 0 T; 17 U; 0 Other;

Query Match 60.8%; Score 58.4; DB 6; Length 95;
Best Local Similarity 82.3%; Pred. No. 1.6e-11;
Matches 79; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

Qy 1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
Db 1 GGGAGAGAGGAAGAGGGAUGGGCACUAUA-CGCAUCUUGCUGCCUGCCCGCGAGUCAAAU 59

Qy 61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
Db 60 UGCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 95

RESULT 8
ABN88497
ID ABN88497 standard; RNA; 96 BP.
XX
AC ABN88497;
XX
DT 19-AUG-2002 (first entry)
XX
DE Coagulation factor IXa binding/inhibiting RNA aptamer SEQ ID NO:10.
XX
KW RNA aptamer; identification; coagulation factor; angiopoietin; thrombin;
KW E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant;
KW cell proliferation; intimal hyperplasia; angiogenesis;
KW bypass graft surgery; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200226932-A2.
XX
PD 04-APR-2002.
XX
PF 26-SEP-2001; 2001WO-US030004.
XX
PR 26-SEP-2000; 2000US-0235654P.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Sullenger BA, Rusconi CP;
XX
DR WPI; 2002-479560/51.
XX
PT Novel RNA aptamers that selectively bind coagulation pathway factors, E2F
PT family members, Ang1 or Ang2, useful for modulating coagulation pathway
PT factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.
XX
PS Claim 13; Fig 1A; 216pp; English.
XX
CC The present invention describes RNA aptamers (I,II,III) that selectively
CC bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c)
CC angiopoietin-1 (Ang1) or Ang2, respectively, where (I), (II), (III) have
CC a dissociation constant for the coagulation pathway factor, an E2F family
CC member, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) have
CC cardiant and cytostatic activities. (I) are useful for modulating the
CC biological activity of a coagulation pathway factor which involves
CC administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that
CC the biological activity of the coagulation pathway factor in the warm-
CC blooded vertebrate is modulated. (I) are also useful for treating
CC cardiovascular diseases in the mammal. (II) are useful for modulating E2F
CC activity in a warm-blooded vertebrate. (III) are useful for modulating
CC Ang1 or Ang2 activity in a warm-blooded vertebrate. (I) are potent
CC anticoagulants and significantly delay the clotting time of normal human
CC plasma or the activation of platelets in response to thrombin. (II) are
CC useful for inhibiting cell proliferation in a number of conditions e.g.,
CC intimal hyperplasia following bypass graft surgery. (III) are useful for
CC modulating angiogenesis. The RNA aptamers are also useful for diagnostic,
CC research and therapeutic context. The aptamers are useful as diagnostic
CC reagents to detect the presence or absence of target substances to which
CC they specifically bind, and for identifying substances to which they
CC specifically bind, for isolating and purifying substances to which they
CC bind, and as a separation reagent for retrieving the targets to which
CC they specifically bind. ABN88488 to ABN88713 and ABB81231 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 96 BP; 30 A; 25 C; 27 G; 0 T; 14 U; 0 Other;

Query Match 58.3%; Score 56; DB 6; Length 96;
Best Local Similarity 74.0%; Pred. No. 1.2e-10;
Matches 71; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Qy 1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
Db 1 GGGAGAGAGGAAGAGGGAUGGGCGAUAUACACAUUGGUGAUCCCACCCACAUGAAACCAC 60

Qy 61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
Db 61 AGCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96

```
RESULT 9
ABN88500
ID   ABN88500 standard; RNA; 96 BP.
XX
AC   ABN88500;
XX
DT   19-AUG-2002  (first entry)
XX
DE   Coagulation factor IXa binding/inhibiting RNA aptamer SEQ ID NO:13.
XX
KW   RNA aptamer; identification; coagulation factor; angiopoietin; thrombin;
KW   E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant;
KW   cell proliferation; intimal hyperplasia; angiogenesis;
KW   bypass graft surgery; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200226932-A2.
XX
PD   04-APR-2002.
XX
PF   26-SEP-2001; 2001WO-US030004.
XX
PR   26-SEP-2000; 2000US-0235654P.
XX
PA   (UYDU-) UNIV DUKE.
XX
PI   Sullenger BA,  Rusconi CP;
XX
DR   WPI; 2002-479560/51.
XX
PT   Novel RNA aptamers that selectively bind coagulation pathway factors, E2F
PT   family members, Ang1 or Ang2, useful for modulating coagulation pathway
PT   factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.
XX
PS   Claim 13; Fig 1B; 216pp; English.
XX
CC   The present invention describes RNA aptamers (I,II,III) that selectively
CC   bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c)
CC   angiopoietin-1 (Ang1) or Ang2, respectively, where (I), (II), (III) have
CC   a dissociation constant for the coagulation pathway factor, an E2F family
CC   member, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) have
CC   cardiant and cytostatic activities. (I) are useful for modulating the
CC   biological activity of a coagulation pathway factor which involves
CC   administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that
CC   the biological activity of the coagulation pathway factor in the warm-
CC   blooded vertebrate is modulated. (I) are also useful for treating
CC   cardiovascular diseases in the mammal. (II) are useful for modulating E2F
CC   activity in a warm-blooded vertebrate. (III) are useful for modulating
CC   Ang1 or Ang2 activity in a warm-blooded vertebrate. (I) are potent
CC   anticoagulants and significantly delay the clotting time of normal human
CC   plasma or the activation of platelets in response to thrombin. (II) are
CC   useful for inhibiting cell proliferation in a number of conditions e.g.,
CC   intimal hyperplasia following bypass graft surgery. (III) are useful for
CC   modulating angiogenesis. The RNA aptamers are also useful for diagnostic,
CC   research and therapeutic context. The aptamers are useful as diagnostic
CC   reagents to detect the presence or absence of target substances to which
CC   they specifically bind, and for identifying substances to which they
CC   specifically bind, for isolating and purifying substances to which they
CC   bind, and as a separation reagent for retrieving the targets to which
CC   they specifically bind. ABN88488 to ABN88713 and ABB81231 represent
CC   sequences used in the exemplification of the present invention
XX
SQ   Sequence 96 BP; 24 A; 29 C; 30 G; 0 T; 13 U; 0 Other;

  Query Match           58.3%;  Score 56;  DB 6;  Length 96;
  Best Local Similarity  74.0%;  Pred. No. 1.2e-10;
  Matches   71;  Conservative    0;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
              ||||||||||||||||||||||  ||    |  | |||  ||  |||  |      | |
Db          1 GGGAGAGAGGAAGAGGGAUGGGCCAUACGUGGACGACUGCACCCGACCCUUCAGCCCAGG 60

Qy         61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
              ||||||||||||||||||||||||||||||||||||
Db         61 UCCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96


RESULT 10
ABN88502
ID   ABN88502 standard; RNA; 96 BP.
XX
AC   ABN88502;
XX
DT   19-AUG-2002  (first entry)
XX
DE   Coagulation factor IXa binding/inhibiting RNA aptamer SEQ ID NO:15.
XX
KW   RNA aptamer; identification; coagulation factor; angiopoietin; thrombin;
KW   E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant;
KW   cell proliferation; intimal hyperplasia; angiogenesis;
KW   bypass graft surgery; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200226932-A2.
XX
PD   04-APR-2002.
XX
PF   26-SEP-2001; 2001WO-US030004.
XX
PR   26-SEP-2000; 2000US-0235654P.
XX
PA   (UYDU-) UNIV DUKE.
XX
PI   Sullenger BA,  Rusconi CP;
XX
DR   WPI; 2002-479560/51.
XX
PT   Novel RNA aptamers that selectively bind coagulation pathway factors, E2F
PT   family members, Ang1 or Ang2, useful for modulating coagulation pathway
PT   factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.
XX
PS   Claim 13; Fig 1B; 216pp; English.
XX
CC   The present invention describes RNA aptamers (I,II,III) that selectively
CC   bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c)
CC   angiopoietin-1 (Ang1) or Ang2, respectively, where (I), (II), (III) have
CC   a dissociation constant for the coagulation pathway factor, an E2F family
CC   member, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) have
CC   cardiant and cytostatic activities. (I) are useful for modulating the
CC   biological activity of a coagulation pathway factor which involves
CC   administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that
CC   the biological activity of the coagulation pathway factor in the warm-
CC   blooded vertebrate is modulated. (I) are also useful for treating
CC   cardiovascular diseases in the mammal. (II) are useful for modulating E2F
CC   activity in a warm-blooded vertebrate. (III) are useful for modulating
CC   Ang1 or Ang2 activity in a warm-blooded vertebrate. (I) are potent
CC   anticoagulants and significantly delay the clotting time of normal human
CC   plasma or the activation of platelets in response to thrombin. (II) are
CC   useful for inhibiting cell proliferation in a number of conditions e.g.,
CC   intimal hyperplasia following bypass graft surgery. (III) are useful for
CC   modulating angiogenesis. The RNA aptamers are also useful for diagnostic,
CC   research and therapeutic context. The aptamers are useful as diagnostic
CC   reagents to detect the presence or absence of target substances to which
CC   they specifically bind, and for identifying substances to which they
CC   specifically bind, for isolating and purifying substances to which they
CC   bind, and as a separation reagent for retrieving the targets to which
CC   they specifically bind. ABN88488 to ABN88713 and ABB81231 represent
CC   sequences used in the exemplification of the present invention
XX
SQ   Sequence 96 BP; 25 A; 25 C; 28 G; 0 T; 17 U; 1 Other;
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  Query Match             57.3%;  Score 55;  DB 6;  Length 96;
  Best Local Similarity   72.9%;  Pred. No. 2.8e-10;
  Matches   70;  Conservative    0;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
              ||||||||||||||||||||    ||  |    |  ||   || |||   ||  |
Db          1 GGGAGAGAGGAAGAGGGAUGGGCCAUAACCACUUUGGUGAACCCACCCAGCUCNUGUGAU 60

Qy         61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
              ||||||||||||||||||||||||||||||||||||
Db         61 UGCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
```

RESULT 11
ABN88527
ID ABN88527 standard; RNA; 96 BP.
XX
AC ABN88527;
XX
DT 19-AUG-2002 (first entry)
XX
DE Coagulation factor VIIa binding/inhibiting RNA aptamer SEQ ID NO:40.
XX
KW RNA aptamer; identification; coagulation factor; angiopoietin; thrombin;
KW E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant;
KW cell proliferation; intimal hyperplasia; angiogenesis;
KW bypass graft surgery; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200226932-A2.
XX
PD 04-APR-2002.
XX
PF 26-SEP-2001; 2001WO-US030004.
XX
PR 26-SEP-2000; 2000US-0235654P.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Sullenger BA, Rusconi CP;
XX
DR WPI; 2002-479560/51.
XX
PT Novel RNA aptamers that selectively bind coagulation pathway factors, E2F
PT family members, Ang1 or Ang2, useful for modulating coagulation pathway
PT factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.
XX
PS Claim 13; Fig 10; 216pp; English.
XX
CC The present invention describes RNA aptamers (I,II,III) that selectively
CC bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c)
CC angiopoietin-1 (Ang1) or Ang2, respectively, where (I), (II), (III) have
CC a dissociation constant for the coagulation pathway factor, an E2F family
CC member, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) have
CC cardiant and cytostatic activities. (I) are useful for modulating the
CC biological activity of a coagulation pathway factor which involves
CC administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that
CC the biological activity of the coagulation pathway factor in the warm-
CC blooded vertebrate is modulated. (I) are also useful for treating
CC cardiovascular diseases in the mammal. (II) are useful for modulating E2F
CC activity in a warm-blooded vertebrate. (III) are useful for modulating
CC Ang1 or Ang2 activity in a warm-blooded vertebrate. (I) are potent
CC anticoagulants and significantly delay the clotting time of normal human
CC plasma or the activation of platelets in response to thrombin. (II) are
CC useful for inhibiting cell proliferation in a number of conditions e.g.,
CC intimal hyperplasia following bypass graft surgery. (III) are useful for
CC modulating angiogenesis. The RNA aptamers are also useful for diagnostic,
CC research and therapeutic context. The aptamers are useful as diagnostic
CC reagents to detect the presence or absence of target substances to which
CC they specifically bind, and for identifying substances to which they
CC specifically bind, for isolating and purifying substances to which they
CC bind, and as a separation reagent for retrieving the targets to which
CC they specifically bind. ABN88488 to ABN88713 and ABB81231 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 96 BP; 28 A; 22 C; 29 G; 0 T; 17 U; 0 Other;

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  Query Match             56.7%;  Score 54.4;  DB 6;  Length 96;
  Best Local Similarity   72.9%;  Pred. No. 4.6e-10;
  Matches   70;  Conservative    0;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
              ||||||||||||||||||||  | | |  || |  ||  |  |  |  ||    |
Db          1 GGGAGAGAGGAAGAGGGAUGGGUGCAAAAGAGCUUCUUGUAGUAUGAUCCCUCAACCGCA 60

Qy         61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
              ||||||||||||||||||||||||||||||||||||
Db         61 AGCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
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RESULT 12
ABN88521
ID ABN88521 standard; RNA; 96 BP.
XX
AC ABN88521;
XX
DT 19-AUG-2002 (first entry)
XX
DE Coagulation factor X binding/inhibiting RNA aptamer SEQ ID NO:34.
XX
KW RNA aptamer; identification; coagulation factor; angiopoietin; thrombin;
KW E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant;
KW cell proliferation; intimal hyperplasia; angiogenesis;
KW bypass graft surgery; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200226932-A2.
XX
PD 04-APR-2002.
XX
PF 26-SEP-2001; 2001WO-US030004.
XX
PR 26-SEP-2000; 2000US-0235654P.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Sullenger BA, Rusconi CP;
XX
DR WPI; 2002-479560/51.
XX
PT Novel RNA aptamers that selectively bind coagulation pathway factors, E2F
PT family members, Ang1 or Ang2, useful for modulating coagulation pathway
PT factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.
XX
PS Claim 13; Fig 6B; 216pp; English.
XX
CC The present invention describes RNA aptamers (I,II,III) that selectively
CC bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c)
CC angiopoietin-1 (Ang1) or Ang2, respectively, where (I), (II), (III) have
CC a dissociation constant for the coagulation pathway factor, an E2F family
CC member, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) have
CC cardiant and cytostatic activities. (I) are useful for modulating the
CC biological activity of a coagulation pathway factor which involves
CC administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that
CC the biological activity of the coagulation pathway factor in the warm-
CC blooded vertebrate is modulated. (I) are also useful for treating
CC cardiovascular diseases in the mammal. (II) are useful for modulating E2F
CC activity in a warm-blooded vertebrate. (III) are useful for modulating
CC Ang1 or Ang2 activity in a warm-blooded vertebrate. (I) are potent
CC anticoagulants and significantly delay the clotting time of normal human
CC plasma or the activation of platelets in response to thrombin. (II) are

CC useful for inhibiting cell proliferation in a number of conditions e.g., CC intimal hyperplasia following bypass graft surgery. (III) are useful for CC modulating angiogenesis. The RNA aptamers are also useful for diagnostic, CC research and therapeutic context. The aptamers are useful as diagnostic CC reagents to detect the presence or absence of target substances to which CC they specifically bind, and for identifying substances to which they CC specifically bind, for isolating and purifying substances to which they CC bind, and as a separation reagent for retrieving the targets to which CC they specifically bind. ABN88488 to ABN88713 and ABB81231 represent CC sequences used in the exemplification of the present invention
XX
SQ Sequence 96 BP; 27 A; 29 C; 29 G; 0 T; 11 U; 0 Other;

Query Match 55.0%; Score 52.8; DB 6; Length 96;
Best Local Similarity 71.9%; Pred. No. 1.8e-09;
Matches 69; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

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              |||||||||||||||||||||      ||||      |       |||| |  |   |
Db          1 GGGAGAGAGGAAGAGGGAUGGGCCAGCAACCGAAGGGCGGAAUACCCCCGUCUCCACAUA 60

Qy         61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
              | ||||||||||||||||||||||||||||||||||
Db         61 CCCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
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RESULT 13
ABN88510
ID ABN88510 standard; RNA; 96 BP.
XX
AC ABN88510;
XX
DT 19-AUG-2002 (first entry)
XX
DE Coagulation factor X binding/inhibiting RNA aptamer SEQ ID NO:23.
XX
KW RNA aptamer; identification; coagulation factor; angiopoietin; thrombin;
KW E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant;
KW cell proliferation; intimal hyperplasia; angiogenesis;
KW bypass graft surgery; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200226932-A2.
XX
PD 04-APR-2002.
XX
PF 26-SEP-2001; 2001WO-US030004.
XX
PR 26-SEP-2000; 2000US-0235654P.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Sullenger BA, Rusconi CP;
XX
DR WPI; 2002-479560/51.
XX
PT Novel RNA aptamers that selectively bind coagulation pathway factors, E2F
PT family members, Ang1 or Ang2, useful for modulating coagulation pathway
PT factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.
XX
PS Claim 13; Fig 6A; 216pp; English.
XX
CC The present invention describes RNA aptamers (I,II,III) that selectively
CC bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c)
CC angiopoietin-1 (Ang1) or Ang2, respectively, where (I), (II), (III) have
CC a dissociation constant for the coagulation pathway factor, an E2F family
CC member, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) have
CC cardiant and cytostatic activities. (I) are useful for modulating the
CC biological activity of a coagulation pathway factor which involves
CC administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that
CC the biological activity of the coagulation pathway factor in the warm-
CC blooded vertebrate is modulated. (I) are also useful for treating
CC cardiovascular diseases in the mammal. (II) are useful for modulating E2F
CC activity in a warm-blooded vertebrate. (III) are useful for modulating
CC Ang1 or Ang2 activity in a warm-blooded vertebrate. (I) are potent
CC anticoagulants and significantly delay the clotting time of normal human
CC plasma or the activation of platelets in response to thrombin. (II) are
CC useful for inhibiting cell proliferation in a number of conditions e.g.,
CC intimal hyperplasia following bypass graft surgery. (III) are useful for
CC modulating angiogenesis. The RNA aptamers are also useful for diagnostic,
CC research and therapeutic context. The aptamers are useful as diagnostic
CC reagents to detect the presence or absence of target substances to which
CC they specifically bind, and for identifying substances to which they
CC specifically bind, for isolating and purifying substances to which they
CC bind, and as a separation reagent for retrieving the targets to which
CC they specifically bind. ABN88488 to ABN88713 and ABB81231 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 96 BP; 29 A; 26 C; 28 G; 0 T; 13 U; 0 Other;

Query Match 53.3%; Score 51.2; DB 6; Length 96;
Best Local Similarity 70.8%; Pred. No. 6.9e-09;
Matches 68; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

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Qy          1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
              |||||||||||||||||||||| |     || |     | |    |      || | ||
Db          1 GGGAGAGAGGAAGAGGGAUGGGAAAAUAGCCCCAGCGAGAUAAUACUUGGCCCCCGUACC 60

Qy         61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
              ||||||||||||||||||||||||||||||||||||
Db         61 ACCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
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RESULT 14
ABN88498
ID ABN88498 standard; RNA; 96 BP.
XX
AC ABN88498;
XX
DT 19-AUG-2002 (first entry)
XX
DE Coagulation factor IXa binding/inhibiting RNA aptamer SEQ ID NO:11.
XX
KW RNA aptamer; identification; coagulation factor; angiopoietin; thrombin;
KW E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant;
KW cell proliferation; intimal hyperplasia; angiogenesis;
KW bypass graft surgery; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200226932-A2.
XX
PD 04-APR-2002.
XX
PF 26-SEP-2001; 2001WO-US030004.
XX
PR 26-SEP-2000; 2000US-0235654P.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Sullenger BA, Rusconi CP;
XX
DR WPI; 2002-479560/51.
XX
PT Novel RNA aptamers that selectively bind coagulation pathway factors, E2F
PT family members, Ang1 or Ang2, useful for modulating coagulation pathway
PT factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.
XX
PS Claim 13; Fig 1A; 216pp; English.
XX
CC The present invention describes RNA aptamers (I,II,III) that selectively
CC bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c)
CC angiopoietin-1 (Ang1) or Ang2, respectively, where (I), (II), (III) have

CC a dissociation constant for the coagulation pathway factor, an E2F family
CC member, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) have
CC cardiant and cytostatic activities. (I) are useful for modulating the
CC biological activity of a coagulation pathway factor which involves
CC administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that
CC the biological activity of the coagulation pathway factor in the warm-
CC blooded vertebrate is modulated. (I) are also useful for treating
CC cardiovascular diseases in the mammal. (II) are useful for modulating E2F
CC activity in a warm-blooded vertebrate. (III) are useful for modulating
CC Ang1 or Ang2 activity in a warm-blooded vertebrate. (I) are potent
CC anticoagulants and significantly delay the clotting time of normal human
CC plasma or the activation of platelets in response to thrombin. (II) are
CC useful for inhibiting cell proliferation in a number of conditions e.g.,
CC intimal hyperplasia following bypass graft surgery. (III) are useful for
CC modulating angiogenesis. The RNA aptamers are also useful for diagnostic,
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CC reagents to detect the presence or absence of target substances to which
CC they specifically bind, and for identifying substances to which they
CC specifically bind, for isolating and purifying substances to which they
CC bind, and as a separation reagent for retrieving the targets to which
CC they specifically bind. ABN88488 to ABN88713 and ABB81231 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 96 BP; 29 A; 24 C; 28 G; 0 T; 13 U; 2 Other;

Query Match 52.9%; Score 50.8; DB 6; Length 96;
Best Local Similarity 69.8%; Pred. No. 9.6e-09;
Matches 67; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
Db 1 GGGAGAGAGGAAGAGGGAUGGGCUCAUCACAGGCGAAGUGAACAACACUACCGNCNAGUU 60

Qy 61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
Db 61 ACCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96

RESULT 15
ABN88501
ID ABN88501 standard; RNA; 96 BP.
XX
AC ABN88501;
XX
DT 19-AUG-2002 (first entry)
XX
DE Coagulation factor IXa binding/inhibiting RNA aptamer SEQ ID NO:14.
XX
KW RNA aptamer; identification; coagulation factor; angiopoietin; thrombin;
KW E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant;
KW cell proliferation; intimal hyperplasia; angiogenesis;
KW bypass graft surgery; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200226932-A2.
XX
PD 04-APR-2002.
XX
PF 26-SEP-2001; 2001WO-US030004.
XX
PR 26-SEP-2000; 2000US-0235654P.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Sullenger BA, Rusconi CP;
XX
DR WPI; 2002-479560/51.
XX
PT Novel RNA aptamers that selectively bind coagulation pathway factors, E2F
PT family members, Ang1 or Ang2, useful for modulating coagulation pathway
PT factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.
XX
PS Claim 13; Fig 1B; 216pp; English.
XX
CC The present invention describes RNA aptamers (I,II,III) that selectively
CC bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c)
CC angiopoietin-1 (Ang1) or Ang2, respectively, where (I), (II), (III) have
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CC cardiant and cytostatic activities. (I) are useful for modulating the
CC biological activity of a coagulation pathway factor which involves
CC administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that
CC the biological activity of the coagulation pathway factor in the warm-
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CC cardiovascular diseases in the mammal. (II) are useful for modulating E2F
CC activity in a warm-blooded vertebrate. (III) are useful for modulating
CC Ang1 or Ang2 activity in a warm-blooded vertebrate. (I) are potent
CC anticoagulants and significantly delay the clotting time of normal human
CC plasma or the activation of platelets in response to thrombin. (II) are
CC useful for inhibiting cell proliferation in a number of conditions e.g.,
CC intimal hyperplasia following bypass graft surgery. (III) are useful for
CC modulating angiogenesis. The RNA aptamers are also useful for diagnostic,
CC research and therapeutic context. The aptamers are useful as diagnostic
CC reagents to detect the presence or absence of target substances to which
CC they specifically bind, and for identifying substances to which they
CC specifically bind, for isolating and purifying substances to which they
CC bind, and as a separation reagent for retrieving the targets to which
CC they specifically bind. ABN88488 to ABN88713 and ABB81231 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 96 BP; 28 A; 28 C; 25 G; 0 T; 15 U; 0 Other;

Query Match 51.7%; Score 49.6; DB 6; Length 96;
Best Local Similarity 69.8%; Pred. No. 2.6e-08;
Matches 67; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

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Db 1 GGGAGAGAGGAAGAGGGAUGGGACCAUACGCACAUUGCUGAAUCCCCCUCAAUAGCACCU 60

Qy 61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
Db 61 ACCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96

Search completed: April 9, 2004, 03:17:44
Job time : 342.082 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 9, 2004, 02:54:20 ; Search time 78.6824 Seconds
(without alignments)
677.093 Million cell updates/sec

Title: US-09-963-827B-3
Perfect score: 96
Sequence: 1 gggagagaggaagagggaug.....cgauaguacuggaucccccc 96

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 979464

Minimum DB seq length: 0
Maximum DB seq length: 200

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	23.6	24.6	87	5	PCT-US95-05600-12	Sequence 12, Appl
	2	21.8	22.7	108	3	US-08-512-861A-3	Sequence 3, Appli
	3	21.8	22.7	109	3	US-08-512-861A-7	Sequence 7, Appli
	4	21.8	22.7	133	3	US-08-512-861A-5	Sequence 5, Appli
	5	21.8	22.7	133	3	US-08-512-861A-9	Sequence 9, Appli
	6	21.8	22.7	146	3	US-08-512-861A-4	Sequence 4, Appli
	7	21.8	22.7	146	3	US-08-512-861A-8	Sequence 8, Appli
	8	21.8	22.7	171	3	US-08-512-861A-6	Sequence 6, Appli
	9	21.8	22.7	171	3	US-08-512-861A-10	Sequence 10, Appl
	10	21.4	22.3	107	4	US-09-581-617-1	Sequence 1, Appli
	11	21.2	22.1	176	4	US-09-919-172-11	Sequence 11, Appl
	12	20.6	21.5	88	3	US-08-512-861A-1	Sequence 1, Appli
	13	20.6	21.5	129	3	US-08-512-861A-13	Sequence 13, Appl
	14	20.6	21.5	167	3	US-08-512-861A-14	Sequence 14, Appl
	15	20.4	21.2	180	1	US-08-443-640-4	Sequence 4, Appli
	16	19.8	20.6	70	3	US-08-512-861A-2	Sequence 2, Appli
	17	19.8	20.6	112	3	US-08-512-861A-15	Sequence 15, Appl
	18	19.8	20.6	112	3	US-08-512-861A-16	Sequence 16, Appl
	19	19.8	20.6	148	3	US-08-512-861A-17	Sequence 17, Appl
	20	19.8	20.6	168	3	US-08-512-861A-18	Sequence 18, Appl
	21	19.6	20.4	131	4	US-08-879-337-11	Sequence 11, Appl
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c	23	19.6	20.4	193	2	US-08-477-504A-40	Sequence 40, Appl
c	24	19.6	20.4	193	2	US-08-486-756A-40	Sequence 40, Appl
c	25	19.6	20.4	193	2	US-08-485-862B-40	Sequence 40, Appl
c	26	19.6	20.4	193	3	US-08-787-739-40	Sequence 40, Appl
c	27	19.6	20.4	193	3	US-08-487-077A-40	Sequence 40, Appl
c	28	19.6	20.4	193	3	US-08-485-863A-40	Sequence 40, Appl
c	29	19.6	20.4	193	3	US-08-485-049D-40	Sequence 40, Appl
c	30	19.6	20.4	193	3	US-09-178-115-40	Sequence 40, Appl
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	32	19.4	20.2	82	5	PCT-US95-05600-14	Sequence 14, Appl
	33	19.4	20.2	87	5	PCT-US95-05600-11	Sequence 11, Appl
	34	19.2	20.0	79	5	PCT-US95-05600-13	Sequence 13, Appl
c	35	18.8	19.6	84	2	US-08-488-402A-97	Sequence 97, Appl
c	36	18.8	19.6	84	2	US-08-484-552A-97	Sequence 97, Appl
c	37	18.8	19.6	84	5	PCT-US96-09472-97	Sequence 97, Appl
	38	18.8	19.6	114	4	US-09-494-921-11	Sequence 11, Appl
	39	18.8	19.6	117	1	US-08-403-762A-94	Sequence 94, Appl
c	40	18.4	19.2	28	5	PCT-US95-05600-3	Sequence 3, Appli
	41	18.4	19.2	68	5	PCT-US95-05600-15	Sequence 15, Appl
	42	18.4	19.2	70	5	PCT-US95-05600-9	Sequence 9, Appli
	43	18.4	19.2	70	5	PCT-US95-05600-10	Sequence 10, Appl
	44	18.4	19.2	71	5	PCT-US95-05600-7	Sequence 7, Appli
	45	18.4	19.2	72	5	PCT-US95-05600-4	Sequence 4, Appli

ALIGNMENTS

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RESULT 1
PCT-US95-05600-12
; Sequence 12, Application PC/TUS9505600
;  GENERAL INFORMATION:
;    APPLICANT:  GOLD, LARRY
;    APPLICANT:  NIEUWLANDT, DAN
;    APPLICANT:  WECKER, MATTHEW
;    APPLICANT:  SCHNEIDER, DANIEL J.
;    APPLICANT:  FEIGON, JULI
;    APPLICANT:  ALLEN, PATRICK
;    APPLICANT:  SULLENGER, BRUCE A.
;    APPLICANT:  DOUDNA, JENNIFER, A.
;    TITLE OF INVENTION:  HIGH-AFFINITY LIGANDS OF
;    TITLE OF INVENTION:  INSULIIN RECEPTOR ANTIBODIES, TACHYKININ SUBSTANCE
;    TITLE OF INVENTION:  P, HIV INTEGRASE AND HIV-1 REVERSE TRANSCRIPTASE
;    NUMBER OF SEQUENCES:  239
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Swanson & Bratschun, L.L.C.
;      STREET:  8400 E. Prentice Avenue, Suite 200
;      CITY:  Englewood
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 MG
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/05600
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/238,863
;      FILING DATE:  06-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/248,632
;      FILING DATE:  24-MAY-1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/303,362
;      FILING DATE:  09-SEPTEMBER-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/361,795
;      FILING DATE:  21-DECEMBER-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/117,991
;      FILING DATE:  08-SEPTEMBER-1993
;    PRIOR APPLICATION DATA:
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;      APPLICATION NUMBER:  07/931,473
;      FILING DATE:  17-AUGUST-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/964,624
;      FILING DATE:  21-OCTOBER-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/536,428
;      FILING DATE:  11-JUNE-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/714,131
;      FILING DATE:  10-JUNE-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/536,428
;      FILING DATE:  11-JUNE-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Barry J. Swanson
;      REGISTRATION NUMBER:  33,215
;      REFERENCE/DOCKET NUMBER:  NEX17/PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 793-3333
;      TELEFAX:  (303) 793-3433
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  87 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
PCT-US95-05600-12

  Query Match             24.6%;  Score 23.6;  DB 5;  Length 87;
  Best Local Similarity   63.1%;  Pred. No. 7.8;
  Matches   53;  Conservative    0;  Mismatches   29;  Indels    2;  Gaps    1;

Qy          1 GGGAGAGAGGAAGAGGGAUGGGGAC--UAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAA 58
              ||||||| ||||| | | ||||  |       |  |||  ||| |  |   | |  |  |
Db          1 GGGAGAGCGGAAGCGUGCUGGGCCCGUGGAGACAUGUAGAGCUUCAACUGAAAUGUGUCA 60

Qy         59 CGCUCAUAACCCAGAGGUCGAUAG 82
              ||  ||||||||||||||||||| |
Db         61 CGAGCAUAACCCAGAGGUCGAUGG 84


RESULT 2
US-08-512-861A-3
; Sequence 3, Application US/08512861A
; Patent No. 6146886
;  GENERAL INFORMATION:
;    APPLICANT:  James D. Thompson
;    TITLE OF INVENTION:  IMPROVED RNA POLYMERASE III-BASED
;    TITLE OF INVENTION:  EXPRESSION OF THERAPEUTIC RNAS
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/512,861A
;      FILING DATE:  August 8, 1995
;    PRIOR APPLICATION DATA:  Two
;      APPLICATION NUMBER:  08/293,520
;      FILING DATE:  August 19, 1994
;      APPLICATION NUMBER:  08/337,608
;      FILING DATE:  No. 6146886ember 10, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  215/154
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  108
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-512-861A-3

  Query Match             22.7%;  Score 21.8;  DB 3;  Length 108;
  Best Local Similarity   58.5%;  Pred. No. 40;
  Matches   38;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy         29 ACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGAUAGUACUGG 88
              || ||  | ||  ||  |   |     |    || ||||||||||||||||||| |  |
Db          7 ACAGCAGAGUGGCGCAGCGGAAGCGUGCUGGGCCCAUAACCCAGAGGUCGAUGGAUCGAA 66

Qy         89 AUCCC 93
              | |||
Db         67 ACCCC 71


RESULT 3
US-08-512-861A-7
; Sequence 7, Application US/08512861A
; Patent No. 6146886
;  GENERAL INFORMATION:
;    APPLICANT:  James D. Thompson
;    TITLE OF INVENTION:  IMPROVED RNA POLYMERASE III-BASED
;    TITLE OF INVENTION:  EXPRESSION OF THERAPEUTIC RNAS
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/512,861A
;      FILING DATE:  August 8, 1995
;    PRIOR APPLICATION DATA:  Two
;      APPLICATION NUMBER:  08/293,520
;      FILING DATE:  August 19, 1994
;      APPLICATION NUMBER:  08/337,608
;      FILING DATE:  No. 6146886ember 10, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  215/154
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  109
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
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;      TOPOLOGY:  linear
US-08-512-861A-7

  Query Match             22.7%;  Score 21.8;  DB 3;  Length 109;
  Best Local Similarity   58.5%;  Pred. No. 41;
  Matches   38;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy          29 ACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGAUAGUACUGG 88
               || ||  | ||  ||  |   |     |    || |||||||||||||||||| | |
Db           7 ACAGCAGAGUGGCGCAGCGGAAGCGUGCUGGGCCCAUAACCCAGAGGUCGAUGGAUCGAA 66

Qy          89 AUCCC 93
               | |||
Db          67 ACCCC 71


RESULT 4
US-08-512-861A-5
; Sequence 5, Application US/08512861A
; Patent No. 6146886
;  GENERAL INFORMATION:
;    APPLICANT:  James D. Thompson
;    TITLE OF INVENTION:  IMPROVED RNA POLYMERASE III-BASED
;    TITLE OF INVENTION:  EXPRESSION OF THERAPEUTIC RNAS
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/512,861A
;      FILING DATE:  August 8, 1995
;    PRIOR APPLICATION DATA:  Two
;      APPLICATION NUMBER:  08/293,520
;      FILING DATE:  August 19, 1994
;      APPLICATION NUMBER:  08/337,608
;      FILING DATE:  No. 6146886ember 10, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  215/154
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  133
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-512-861A-5

  Query Match             22.7%;  Score 21.8;  DB 3;  Length 133;
  Best Local Similarity   58.5%;  Pred. No. 43;
  Matches   38;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy          29 ACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGAUAGUACUGG 88
               || ||  | ||  ||  |   |     |    || |||||||||||||||||| | |
Db           7 ACAGCAGAGUGGCGCAGCGGAAGCGUGCUGGGCCCAUAACCCAGAGGUCGAUGGAUCGAA 66

Qy          89 AUCCC 93
               | |||
Db          67 ACCCC 71


RESULT 5
US-08-512-861A-9
; Sequence 9, Application US/08512861A
; Patent No. 6146886
;  GENERAL INFORMATION:
;    APPLICANT:  James D. Thompson
;    TITLE OF INVENTION:  IMPROVED RNA POLYMERASE III-BASED
;    TITLE OF INVENTION:  EXPRESSION OF THERAPEUTIC RNAS
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/512,861A
;      FILING DATE:  August 8, 1995
;    PRIOR APPLICATION DATA:  Two
;      APPLICATION NUMBER:  08/293,520
;      FILING DATE:  August 19, 1994
;      APPLICATION NUMBER:  08/337,608
;      FILING DATE:  No. 6146886ember 10, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  215/154
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  133
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-512-861A-9

  Query Match             22.7%;  Score 21.8;  DB 3;  Length 133;
  Best Local Similarity   58.5%;  Pred. No. 43;
  Matches   38;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy          29 ACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGAUAGUACUGG 88
               || ||  | ||  ||  |   |     |    || |||||||||||||||||| | |
Db           7 ACAGCAGAGUGGCGCAGCGGAAGCGUGCUGGGCCCAUAACCCAGAGGUCGAUGGAUCGAA 66

Qy          89 AUCCC 93
               | |||
Db          67 ACCCC 71


RESULT 6
US-08-512-861A-4
; Sequence 4, Application US/08512861A
; Patent No. 6146886
;  GENERAL INFORMATION:
;    APPLICANT:  James D. Thompson
;    TITLE OF INVENTION:  IMPROVED RNA POLYMERASE III-BASED
;    TITLE OF INVENTION:  EXPRESSION OF THERAPEUTIC RNAS
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
```

```
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/512,861A
;      FILING DATE:  August 8, 1995
;    PRIOR APPLICATION DATA:  Two
;      APPLICATION NUMBER:  08/293,520
;      FILING DATE:  August 19, 1994
;      APPLICATION NUMBER:  08/337,608
;      FILING DATE:  No. 6146886ember 10, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  215/154
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  146
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-512-861A-4

  Query Match             22.7%;  Score 21.8;  DB 3;  Length 146;
  Best Local Similarity   58.5%;  Pred. No. 45;
  Matches   38;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy          29 ACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGAUAGUACUGG 88
               || ||  | ||  ||  |   |     |    || ||||||||||||||||||  |  |
Db           7 ACAGCAGAGUGGCGCAGCGGAAGCGUGCUGGGCCCAUAACCCAGAGGUCGAUGGAUCGAA 66

Qy          89 AUCCC 93
               | |||
Db          67 ACCCC 71


RESULT 7
US-08-512-861A-8
; Sequence 8, Application US/08512861A
; Patent No. 6146886
;  GENERAL INFORMATION:
;    APPLICANT:  James D. Thompson
;    TITLE OF INVENTION:  IMPROVED RNA POLYMERASE III-BASED
;    TITLE OF INVENTION:  EXPRESSION OF THERAPEUTIC RNAS
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/512,861A
;      FILING DATE:  August 8, 1995
;    PRIOR APPLICATION DATA:  Two
;      APPLICATION NUMBER:  08/293,520
;      FILING DATE:  August 19, 1994
;      APPLICATION NUMBER:  08/337,608
;      FILING DATE:  No. 6146886ember 10, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  215/154
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  146
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-512-861A-8

  Query Match             22.7%;  Score 21.8;  DB 3;  Length 146;
  Best Local Similarity   58.5%;  Pred. No. 45;
  Matches   38;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy          29 ACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGAUAGUACUGG 88
               || ||  | ||  ||  |   |     |    || ||||||||||||||||||  |  |
Db           7 ACAGCAGAGUGGCGCAGCGGAAGCGUGCUGGGCCCAUAACCCAGAGGUCGAUGGAUCGAA 66

Qy          89 AUCCC 93
               | |||
Db          67 ACCCC 71


RESULT 8
US-08-512-861A-6
; Sequence 6, Application US/08512861A
; Patent No. 6146886
;  GENERAL INFORMATION:
;    APPLICANT:  James D. Thompson
;    TITLE OF INVENTION:  IMPROVED RNA POLYMERASE III-BASED
;    TITLE OF INVENTION:  EXPRESSION OF THERAPEUTIC RNAS
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/512,861A
;      FILING DATE:  August 8, 1995
;    PRIOR APPLICATION DATA:  Two
;      APPLICATION NUMBER:  08/293,520
;      FILING DATE:  August 19, 1994
;      APPLICATION NUMBER:  08/337,608
;      FILING DATE:  No. 6146886ember 10, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  215/154
;    TELECOMMUNICATION INFORMATION:
```

```
;       TELEPHONE:  (213) 489-1600
;       TELEFAX:  (213) 955-0440
;       TELEX:  67-3510
;     INFORMATION FOR SEQ ID NO:  6:
;       SEQUENCE CHARACTERISTICS:
;         LENGTH:  171
;         TYPE:  nucleic acid
;         STRANDEDNESS:  single
;         TOPOLOGY:  linear
US-08-512-861A-6

  Query Match           22.7%;  Score 21.8;  DB 3;  Length 171;
  Best Local Similarity  58.5%;  Pred. No. 47;
  Matches   38;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy         29 ACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGAUAGUACUGG 88
              || ||  | ||  ||  |   |    |   || ||||||||||||||||||  |  |
Db          7 ACAGCAGAGUGGCGCAGCGGAAGCGUGCUGGGCCCAUAACCCAGAGGUCGAUGGAUCGAA 66

Qy         89 AUCCC 93
              | |||
Db         67 ACCCC 71


RESULT 9
US-08-512-861A-10
; Sequence 10, Application US/08512861A
; Patent No. 6146886
;  GENERAL INFORMATION:
;    APPLICANT:  James D. Thompson
;    TITLE OF INVENTION:  IMPROVED RNA POLYMERASE III-BASED
;    TITLE OF INVENTION:  EXPRESSION OF THERAPEUTIC RNAS
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/512,861A
;      FILING DATE:  August 8, 1995
;    PRIOR APPLICATION DATA:  Two
;      APPLICATION NUMBER:  08/293,520
;      FILING DATE:  August 19, 1994
;      APPLICATION NUMBER:  08/337,608
;      FILING DATE:  No. 6146886ember 10, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  215/154
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  171
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-512-861A-10

  Query Match           22.7%;  Score 21.8;  DB 3;  Length 171;
  Best Local Similarity  58.5%;  Pred. No. 47;
  Matches   38;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy         29 ACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGAUAGUACUGG 88
              || ||  | ||  ||  |   |    |   || ||||||||||||||||||  |  |
Db          7 ACAGCAGAGUGGCGCAGCGGAAGCGUGCUGGGCCCAUAACCCAGAGGUCGAUGGAUCGAA 66

Qy         89 AUCCC 93
              | |||
Db         67 ACCCC 71


RESULT 10
US-09-581-617-1
; Sequence 1, Application US/09581617
; Patent No. 6346385
; GENERAL INFORMATION:
;  APPLICANT:  Teijin Limited
;  TITLE OF INVENTION:  Analysis of predisposition based on human airway
;  TITLE OF INVENTION:  tripsin protease gene polymorphism
;  FILE REFERENCE:  Q59572
;  CURRENT APPLICATION NUMBER: US/09/581,617
;  CURRENT FILING DATE:  2000-06-15
;  PRIOR APPLICATION NUMBER:  PCT/JP98/05689
;  PRIOR FILING DATE:  1998-12-16
;  PRIOR APPLICATION NUMBER:  9-346494 JAPAN
;  PRIOR FILING DATE:  1997-12-16
;  NUMBER OF SEQ ID NOS:  17
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 107
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-581-617-1

  Query Match           22.3%;  Score 21.4;  DB 4;  Length 107;
  Best Local Similarity  50.9%;  Pred. No. 57;
  Matches   28;  Conservative    6;  Mismatches   21;  Indels    0;  Gaps    0;

Qy         40 CUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCC 94
              |: ||: ||||:   |||||  : | ||   | |||:|   |  ||:| | || |
Db         13 CTACCTACCCATCTGGGAACAATTAGAATAGACAGGTCATGAAGACTGCACCCTC 67


RESULT 11
US-09-919-172-11
; Sequence 11, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
;  APPLICANT: Faris, Mary
;  APPLICANT:  Turner, Christopher M.
;  TITLE OF INVENTION: PROSTATE CANCER MARKERS
;  FILE REFERENCE: PA-0036 US
;  CURRENT APPLICATION NUMBER: US/09/919,172
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: 60/222,469
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PERL Program
; SEQ ID NO 11
;   LENGTH: 176
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6673545 378497.1
;   NAME/KEY: unsure
;   LOCATION: 18, 30, 35, 39, 44, 52, 87, 93, 108, 112, 114, 151, 166, 168, 170
;   OTHER INFORMATION: a, t, c, g, or other
US-09-919-172-11

  Query Match           22.1%;  Score 21.2;  DB 4;  Length 176;
  Best Local Similarity  46.8%;  Pred. No. 80;
  Matches   29;  Conservative    6;  Mismatches   27;  Indels    0;  Gaps    0;
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Qy          19 UGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCG 78
               :|  ||    || | | | : | | |: ||| : || | ||| :||   ||||| |   |
Db          94 TGAAGAGATGACGGNGCANTNCCGGCTTCCCTTCCCCGCACGGTCAGGCCCCAGTGTNAG 153

Qy          79 AU 80
               :
Db         154 GT 155


RESULT 12
US-08-512-861A-1
; Sequence 1, Application US/08512861A
; Patent No. 6146886
;  GENERAL INFORMATION:
;    APPLICANT:  James D. Thompson
;    TITLE OF INVENTION:  IMPROVED RNA POLYMERASE III-BASED
;    TITLE OF INVENTION:  EXPRESSION OF THERAPEUTIC RNAS
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/512,861A
;      FILING DATE:  August 8, 1995
;    PRIOR APPLICATION DATA:  Two
;      APPLICATION NUMBER:  08/293,520
;      FILING DATE:  August 19, 1994
;      APPLICATION NUMBER:  08/337,608
;      FILING DATE:  No. 6146886ember 10, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  215/154
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  88
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-512-861A-1

  Query Match             21.5%;  Score 20.6;  DB 3;  Length 88;
  Best Local Similarity   56.7%;  Pred. No. 1.1e+02;
  Matches   38;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          29 ACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGAUAGUACUGG 88
               || ||  | ||  ||  |   |     |   || ||||||||||||||||||  |   |
Db           7 ACAGCAGAGUGGCGCAGCGGAAGCGUGCUGGGCCCAUAACCCAGAGGUCGAUGGAUCGAA 66

Qy          89 AUCCCCC 95
               | |  ||
Db          67 ACCAUCC 73


RESULT 13
US-08-512-861A-13
; Sequence 13, Application US/08512861A
; Patent No. 6146886
;  GENERAL INFORMATION:
;    APPLICANT:  James D. Thompson
;    TITLE OF INVENTION:  IMPROVED RNA POLYMERASE III-BASED
;    TITLE OF INVENTION:  EXPRESSION OF THERAPEUTIC RNAS
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/512,861A
;      FILING DATE:  August 8, 1995
;    PRIOR APPLICATION DATA:  Two
;      APPLICATION NUMBER:  08/293,520
;      FILING DATE:  August 19, 1994
;      APPLICATION NUMBER:  08/337,608
;      FILING DATE:  No. 6146886ember 10, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  215/154
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  129
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-512-861A-13

  Query Match             21.5%;  Score 20.6;  DB 3;  Length 129;
  Best Local Similarity   56.7%;  Pred. No. 1.2e+02;
  Matches   38;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          29 ACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGAUAGUACUGG 88
               || ||  | ||  ||  |   |     |   || ||||||||||||||||||  |   |
Db           7 ACAGCAGAGUGGCGCAGCGGAAGCGUGCUGGGCCCAUAACCCAGAGGUCGAUGGAUCGAA 66

Qy          89 AUCCCCC 95
               | |  ||
Db          67 ACCAUCC 73


RESULT 14
US-08-512-861A-14
; Sequence 14, Application US/08512861A
; Patent No. 6146886
;  GENERAL INFORMATION:
;    APPLICANT:  James D. Thompson
;    TITLE OF INVENTION:  IMPROVED RNA POLYMERASE III-BASED
;    TITLE OF INVENTION:  EXPRESSION OF THERAPEUTIC RNAS
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
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;       ZIP:  90071
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;       MEDIUM TYPE:  storage
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  IBM P.C. DOS 5.0
;       SOFTWARE:  FastSEQ Version 1.5
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/512,861A
;       FILING DATE:  August 8, 1995
;     PRIOR APPLICATION DATA:  Two
;       APPLICATION NUMBER:  08/293,520
;       FILING DATE:  August 19, 1994
;       APPLICATION NUMBER:  08/337,608
;       FILING DATE:  No. 6146886ember 10, 1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Warburg, Richard
;       REGISTRATION NUMBER:  32,327
;       REFERENCE/DOCKET NUMBER:  215/154
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (213) 489-1600
;       TELEFAX:  (213) 955-0440
;       TELEX:  67-3510
;   INFORMATION FOR SEQ ID NO:  14:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  167
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-512-861A-14

  Query Match             21.5%;  Score 20.6;  DB 3;  Length 167;
  Best Local Similarity   56.7%;  Pred. No. 1.3e+02;
  Matches   38;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          29 ACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGAUAGUACUGG 88
               || ||  | ||  ||  |   |     |    || ||||||||||||||||||  |  |
Db           7 ACAGCAGAGUGGCGCAGCGGAAGCGUGCUGGGCCCAUAACCCAGAGGUCGAUGGAUCGAA 66

Qy          89 AUCCCCC 95
               | |  ||
Db          67 ACCAUCC 73


RESULT 15
US-08-443-640-4
; Sequence 4, Application US/08443640
; Patent No. 5691140
;  GENERAL INFORMATION:
;    APPLICANT:  NOREN, CHRISTOPHER J.
;    APPLICANT:  EVANS, PAUL D.
;    TITLE OF INVENTION:  BIDIRECTIONAL IN VITRO TRANSCRIPTION
;    TITLE OF INVENTION:  VECTORS UTILIZING A SINGLE RNA POLYMERASE FOR BOTH
;    TITLE OF INVENTION:  DIRECTIONS
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NEW ENGLAND BIOLABS, INC
;      STREET:  32 TOZER ROAD
;      CITY:  BEVERLY
;      STATE:  MASSACHUSETTS
;      COUNTRY:  US
;      ZIP:  01915
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/443,640
;      FILING DATE:  18-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WILLIAMS, GREGORY D.
;      REGISTRATION NUMBER:  30901
;      REFERENCE/DOCKET NUMBER:  NEB-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (508) 927-5054
;      TELEFAX:  (508) 927-1705
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-08-443-640-4

  Query Match             21.2%;  Score 20.4;  DB 1;  Length 180;
  Best Local Similarity   46.3%;  Pred. No. 1.6e+02;
  Matches   25;  Conservative    8;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          41 UGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCC 94
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Db          37 TGCCTGTACACTCCGGAAGACGCGTTCGGCCGTGCTAGCGAATTCTGGATCCAC 90


Search completed:  April  9, 2004, 06:07:31
Job time :  81.6824 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 9, 2004, 03:53:35 ; Search time 1188.14 Seconds
(without alignments)
303.112 Million cell updates/sec

Title: US-09-963-827B-3
Perfect score: 96
Sequence: 1 gggagagaggaagagggaug.....cgauaguacuggaucccccc 96

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2475585 seqs, 1875730760 residues

Total number of hits satisfying chosen parameters: 1817818

Minimum DB seq length: 0
Maximum DB seq length: 200

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	96	100.0	96	10	US-09-963-827B-3	Sequence 3, Appli
2	62	64.6	94	10	US-09-963-827B-19	Sequence 19, Appl
3	60.8	63.3	96	10	US-09-963-827B-17	Sequence 17, Appl
4	60	62.5	95	10	US-09-963-827B-22	Sequence 22, Appl
5	59.2	61.7	96	10	US-09-963-827B-2	Sequence 2, Appli
6	58.4	60.8	95	10	US-09-963-827B-4	Sequence 4, Appli
7	58.4	60.8	95	10	US-09-963-827B-12	Sequence 12, Appl
8	56	58.3	96	10	US-09-963-827B-10	Sequence 10, Appl
9	56	58.3	96	10	US-09-963-827B-13	Sequence 13, Appl
10	55	57.3	96	10	US-09-963-827B-15	Sequence 15, Appl
11	54.4	56.7	96	10	US-09-963-827B-40	Sequence 40, Appl
12	51.2	53.3	96	10	US-09-963-827B-23	Sequence 23, Appl
13	50.8	52.9	96	10	US-09-963-827B-11	Sequence 11, Appl
14	49.6	51.7	96	10	US-09-963-827B-6	Sequence 6, Appli
15	49.6	51.7	96	10	US-09-963-827B-9	Sequence 9, Appli
16	49.6	51.7	96	10	US-09-963-827B-14	Sequence 14, Appl
17	49.6	51.7	96	10	US-09-963-827B-16	Sequence 16, Appl
18	49.6	51.7	96	10	US-09-963-827B-39	Sequence 39, Appl
19	49.6	51.7	96	10	US-09-963-827B-41	Sequence 41, Appl
20	49.6	51.7	96	10	US-09-963-827B-44	Sequence 44, Appl
21	48	50.0	96	10	US-09-963-827B-21	Sequence 21, Appl
22	48	50.0	96	10	US-09-963-827B-42	Sequence 42, Appl
23	48	50.0	96	10	US-09-963-827B-43	Sequence 43, Appl
24	47.2	49.2	92	10	US-09-963-827B-73	Sequence 73, Appl
25	47.2	49.2	95	10	US-09-963-827B-20	Sequence 20, Appl
26	47.2	49.2	95	10	US-09-963-827B-28	Sequence 28, Appl
27	46.6	48.5	97	10	US-09-963-827B-24	Sequence 24, Appl
28	46.4	48.3	96	10	US-09-963-827B-5	Sequence 5, Appli
29	46.4	48.3	96	10	US-09-963-827B-18	Sequence 18, Appl
30	46.4	48.3	96	10	US-09-963-827B-45	Sequence 45, Appl
31	46.4	48.3	96	10	US-09-963-827B-46	Sequence 46, Appl
32	46.4	48.3	96	10	US-09-963-827B-47	Sequence 47, Appl
33	46.2	48.1	99	10	US-09-963-827B-31	Sequence 31, Appl
34	45	46.9	97	10	US-09-963-827B-27	Sequence 27, Appl
35	45	46.9	97	10	US-09-963-827B-34	Sequence 34, Appl
36	45	46.9	97	10	US-09-963-827B-36	Sequence 36, Appl
37	44.8	46.7	96	10	US-09-963-827B-7	Sequence 7, Appli
38	43.4	45.2	92	10	US-09-963-827B-25	Sequence 25, Appl
39	43.4	45.2	97	10	US-09-963-827B-32	Sequence 32, Appl
40	43.2	45.0	96	10	US-09-963-827B-1	Sequence 1, Appli
41	41.8	43.5	97	10	US-09-963-827B-26	Sequence 26, Appl
42	41.8	43.5	97	10	US-09-963-827B-29	Sequence 29, Appl
43	40.4	42.1	100	10	US-09-963-827B-33	Sequence 33, Appl
44	40.2	41.9	97	10	US-09-963-827B-37	Sequence 37, Appl
45	40	41.7	40	14	US-10-155-233-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-963-827B-3
; Sequence 3, Application US/09963827B
; Publication No. US20030175703A1
; GENERAL INFORMATION:
; APPLICANT: Duke University
; APPLICANT: Sullenger, Bruce
; APPLICANT: Rusconi, Christopher
; TITLE OF INVENTION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME
; FILE REFERENCE: 180/124/2
; CURRENT APPLICATION NUMBER: US/09/963,827B
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,654
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 96
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: RNA aptamer
; FEATURE:
; NAME/KEY: RNA aptamer
; LOCATION: (1)..(96)
; OTHER INFORMATION: RNA aptamer
US-09-963-827B-3

Query Match 100.0%; Score 96; DB 10; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.5e-26;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60

Qy         61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
              |||||||||||||||||||||||||||||||||||||
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Db         61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96


RESULT 2
US-09-963-827B-19
; Sequence 19, Application US/09963827B
; Publication No. US20030175703A1
; GENERAL INFORMATION:
;  APPLICANT: Duke University
;  APPLICANT:  Sullenger, Bruce
;  APPLICANT:  Rusconi, Christopher
;  TITLE OF INVENTION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME
;  FILE REFERENCE: 180/124/2
;  CURRENT APPLICATION NUMBER: US/09/963,827B
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 60/235,654
;  PRIOR FILING DATE: 2000-09-26
;  NUMBER OF SEQ ID NOS: 227
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
;   LENGTH: 94
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: RNA aptamer
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(94)
;   OTHER INFORMATION: RNA aptamer
US-09-963-827B-19

  Query Match             64.6%;  Score 62;  DB 10;  Length 94;
  Best Local Similarity   78.7%;  Pred. No. 1.2e-13;
  Matches   74;  Conservative    0;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCCAUUCCGGAACG 60
              |||||||||||||||||||||||||| ||| | |  |  | ||  ||||   ||  ||
Db          1 GGGAGAGAGGAAGAGGGAUGGGGACCAUAACUCUAACGGGUGAAUCCCGCAUCUCGACAA 60

Qy         61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCC 94
              ||||||||||||||||||||||||||||||||||
Db         61 UACAUAACCCAGAGGUCGAUAGUACUGGAUCCCC 94


RESULT 3
US-09-963-827B-17
; Sequence 17, Application US/09963827B
; Publication No. US20030175703A1
; GENERAL INFORMATION:
;  APPLICANT: Duke University
;  APPLICANT:  Sullenger, Bruce
;  APPLICANT:  Rusconi, Christopher
;  TITLE OF INVENTION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME
;  FILE REFERENCE: 180/124/2
;  CURRENT APPLICATION NUMBER: US/09/963,827B
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 60/235,654
;  PRIOR FILING DATE: 2000-09-26
;  NUMBER OF SEQ ID NOS: 227
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
;   LENGTH: 96
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: RNA aptamer
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(96)
;   OTHER INFORMATION: RNA aptamer
US-09-963-827B-17

  Query Match             63.3%;  Score 60.8;  DB 10;  Length 96;
  Best Local Similarity   77.1%;  Pred. No. 3.4e-13;
  Matches   74;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

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              |||||||||||||||||||||||||||||||||||||    |  |       |||    ||  |
Db          1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGGCAAUCGUGCAUCCCCUGGACCUAACAA 60

Qy         61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
              ||||||||||||||||||||||||||||||||||||
Db         61 UACAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96


RESULT 4
US-09-963-827B-22
; Sequence 22, Application US/09963827B
; Publication No. US20030175703A1
; GENERAL INFORMATION:
;  APPLICANT: Duke University
;  APPLICANT:  Sullenger, Bruce
;  APPLICANT:  Rusconi, Christopher
;  TITLE OF INVENTION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME
;  FILE REFERENCE: 180/124/2
;  CURRENT APPLICATION NUMBER: US/09/963,827B
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 60/235,654
;  PRIOR FILING DATE: 2000-09-26
;  NUMBER OF SEQ ID NOS: 227
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
;   LENGTH: 95
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: RNA aptamer
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(95)
;   OTHER INFORMATION: RNA aptamer
US-09-963-827B-22

  Query Match             62.5%;  Score 60;  DB 10;  Length 95;
  Best Local Similarity   83.3%;  Pred. No. 6.8e-13;
  Matches   80;  Conservative    0;  Mismatches   15;  Indels    1;  Gaps    1;

Qy          1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
              |||||||||||||||||||||||  | ||| |||  | |||||| || || | ||| ||
Db          1 GGGAGAGAGGAAGAGGGAUGGGCGCCAUA-CGCACAUUGCUGCAUCGCCUUCCCGUAAGA 59

Qy         61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
              ||||||||||||||||||||||||||||||||||||
Db         60 ACCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 95


RESULT 5
US-09-963-827B-2
; Sequence 2, Application US/09963827B
; Publication No. US20030175703A1
; GENERAL INFORMATION:
;  APPLICANT: Duke University
;  APPLICANT:  Sullenger, Bruce
;  APPLICANT:  Rusconi, Christopher
;  TITLE OF INVENTION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME
;  FILE REFERENCE: 180/124/2
;  CURRENT APPLICATION NUMBER: US/09/963,827B
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 60/235,654
;  PRIOR FILING DATE: 2000-09-26
;  NUMBER OF SEQ ID NOS: 227
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 96
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
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;   FEATURE:
;   OTHER INFORMATION: RNA aptamer
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(96)
;   OTHER INFORMATION: RNA aptamer
US-09-963-827B-2

  Query Match             61.7%;  Score 59.2;  DB 10;  Length 96;
  Best Local Similarity   76.0%;  Pred. No. 1.4e-12;
  Matches   73;  Conservative    0;  Mismatches   23;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||   |||||    |  || | ||  | || |    |
Db          1 GGGAGAGAGGAAGAGGGAUGGGCUAUAUACACGCUGGUGAUCCCAUCUCAAUUGAAACAA 60

Qy         61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
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RESULT 6
US-09-963-827B-4
; Sequence 4, Application US/09963827B
; Publication No. US20030175703A1
; GENERAL INFORMATION:
;  APPLICANT: Duke University
;  APPLICANT:  Sullenger, Bruce
;  APPLICANT:  Rusconi, Christopher
;  TITLE OF INVENTION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME
;  FILE REFERENCE: 180/124/2
;  CURRENT APPLICATION NUMBER: US/09/963,827B
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 60/235,654
;  PRIOR FILING DATE: 2000-09-26
;  NUMBER OF SEQ ID NOS: 227
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 95
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: RNA aptamer
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(95)
;   OTHER INFORMATION: RNA aptamer
US-09-963-827B-4

  Query Match             60.8%;  Score 58.4;  DB 10;  Length 95;
  Best Local Similarity   82.3%;  Pred. No. 2.7e-12;
  Matches   79;  Conservative    0;  Mismatches   16;  Indels    1;  Gaps    1;

Qy          1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
              |||||||||||||||||||| |||||| ||| |  |||||||| |||       ||
Db          1 GGGAGAGAGGAAGAGGGAUGGGCACUAUA-CGCAUCUUGCUGCCUGCCCGCGAGUCAAAU 59

Qy         61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
              ||||||||||||||||||||||||||||||||||||
Db         60 UGCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 95


RESULT 7
US-09-963-827B-12
; Sequence 12, Application US/09963827B
; Publication No. US20030175703A1
; GENERAL INFORMATION:
;  APPLICANT: Duke University
;  APPLICANT:  Sullenger, Bruce
;  APPLICANT:  Rusconi, Christopher
;  TITLE OF INVENTION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME
;  FILE REFERENCE: 180/124/2
;  CURRENT APPLICATION NUMBER: US/09/963,827B
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 60/235,654
;  PRIOR FILING DATE: 2000-09-26
;  NUMBER OF SEQ ID NOS: 227
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
;   LENGTH: 95
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: RNA aptamer
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(95)
;   OTHER INFORMATION: RNA aptamer
US-09-963-827B-12

  Query Match             60.8%;  Score 58.4;  DB 10;  Length 95;
  Best Local Similarity   82.3%;  Pred. No. 2.7e-12;
  Matches   79;  Conservative    0;  Mismatches   16;  Indels    1;  Gaps    1;

Qy          1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
              |||||||||||||||||||||||||||||| || | |   |||| ||| | | || |
Db          1 GGGAGAGAGGAAGAGGGAUGGGGACUAUA-CGUGAACGACUGCAUCCACUUCCCCGCCAU 59

Qy         61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
              ||||||||||||||||||||||||||||||||||||
Db         60 GGCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 95


RESULT 8
US-09-963-827B-10
; Sequence 10, Application US/09963827B
; Publication No. US20030175703A1
; GENERAL INFORMATION:
;  APPLICANT: Duke University
;  APPLICANT:  Sullenger, Bruce
;  APPLICANT:  Rusconi, Christopher
;  TITLE OF INVENTION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME
;  FILE REFERENCE: 180/124/2
;  CURRENT APPLICATION NUMBER: US/09/963,827B
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 60/235,654
;  PRIOR FILING DATE: 2000-09-26
;  NUMBER OF SEQ ID NOS: 227
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
;   LENGTH: 96
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: RNA aptamer
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(96)
;   OTHER INFORMATION: RNA aptamer
US-09-963-827B-10

  Query Match             58.3%;  Score 56;  DB 10;  Length 96;
  Best Local Similarity   74.0%;  Pred. No. 2.2e-11;
  Matches   71;  Conservative    0;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
              ||||||||||||||||||||   |||||    |  || | || |||   |
Db          1 GGGAGAGAGGAAGAGGGAUGGGCGAUAUACACAUUGGUGAUCCCACCCACAUGAAACCAC 60

Qy         61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
              ||||||||||||||||||||||||||||||||||||
Db         61 AGCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96


RESULT 9
US-09-963-827B-13
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; Sequence 13, Application US/09963827B
; Publication No. US20030175703A1
; GENERAL INFORMATION:
;  APPLICANT: Duke University
;  APPLICANT:  Sullenger, Bruce
;  APPLICANT:  Rusconi, Christopher
;  TITLE OF INVENTION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME
;  FILE REFERENCE: 180/124/2
;  CURRENT APPLICATION NUMBER: US/09/963,827B
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 60/235,654
;  PRIOR FILING DATE: 2000-09-26
;  NUMBER OF SEQ ID NOS: 227
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
;   LENGTH: 96
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: RNA aptamer
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(96)
;   OTHER INFORMATION: RNA aptamer
US-09-963-827B-13

  Query Match             58.3%;  Score 56;  DB 10;  Length 96;
  Best Local Similarity   74.0%;  Pred. No. 2.2e-11;
  Matches   71;  Conservative    0;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
              ||||||||||||||||||||    ||     |   | |||  ||  ||| |       | |
Db          1 GGGAGAGAGGAAGAGGGAUGGGCCAUACGUGGACGACUGCACCCGACCCUUCAGCCCAGG 60

Qy         61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
              ||||||||||||||||||||||||||||||||||||
Db         61 UCCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96


RESULT 10
US-09-963-827B-15
; Sequence 15, Application US/09963827B
; Publication No. US20030175703A1
; GENERAL INFORMATION:
;  APPLICANT: Duke University
;  APPLICANT:  Sullenger, Bruce
;  APPLICANT:  Rusconi, Christopher
;  TITLE OF INVENTION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME
;  FILE REFERENCE: 180/124/2
;  CURRENT APPLICATION NUMBER: US/09/963,827B
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 60/235,654
;  PRIOR FILING DATE: 2000-09-26
;  NUMBER OF SEQ ID NOS: 227
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
;   LENGTH: 96
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: RNA aptamer
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (54)..(54)
;   OTHER INFORMATION: n=c or u
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(96)
;   OTHER INFORMATION: RNA aptamer
US-09-963-827B-15

  Query Match             57.3%;  Score 55;  DB 10;  Length 96;
  Best Local Similarity   72.9%;  Pred. No. 5.3e-11;
  Matches   70;  Conservative    0;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
              ||||||||||||||||||||    ||  |    |  ||   || |||   ||  |
Db          1 GGGAGAGAGGAAGAGGGAUGGGCCAUAACCACUUUGGUGAACCCACCCAGCUCNUGUGAU 60

Qy         61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
              ||||||||||||||||||||||||||||||||||||
Db         61 UGCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96


RESULT 11
US-09-963-827B-40
; Sequence 40, Application US/09963827B
; Publication No. US20030175703A1
; GENERAL INFORMATION:
;  APPLICANT: Duke University
;  APPLICANT:  Sullenger, Bruce
;  APPLICANT:  Rusconi, Christopher
;  TITLE OF INVENTION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME
;  FILE REFERENCE: 180/124/2
;  CURRENT APPLICATION NUMBER: US/09/963,827B
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 60/235,654
;  PRIOR FILING DATE: 2000-09-26
;  NUMBER OF SEQ ID NOS: 227
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40
;   LENGTH: 96
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: RNA aptamer
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(96)
;   OTHER INFORMATION: RNA aptamer
US-09-963-827B-40

  Query Match             56.7%;  Score 54.4;  DB 10;  Length 96;
  Best Local Similarity   72.9%;  Pred. No. 9e-11;
  Matches   70;  Conservative    0;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          1 GGGAGAGAGGAAGAGGGAUGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
              ||||||||||||||||||||  | | |  || |  ||  |  |  |  ||     |
Db          1 GGGAGAGAGGAAGAGGGAUGGGUGCAAAAGAGCUUCUUGUAGUAUGAUCCCUCAACCGCA 60

Qy         61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
              ||||||||||||||||||||||||||||||||||||
Db         61 AGCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96


RESULT 12
US-09-963-827B-23
; Sequence 23, Application US/09963827B
; Publication No. US20030175703A1
; GENERAL INFORMATION:
;  APPLICANT: Duke University
;  APPLICANT:  Sullenger, Bruce
;  APPLICANT:  Rusconi, Christopher
;  TITLE OF INVENTION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME
;  FILE REFERENCE: 180/124/2
;  CURRENT APPLICATION NUMBER: US/09/963,827B
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 60/235,654
;  PRIOR FILING DATE: 2000-09-26
;  NUMBER OF SEQ ID NOS: 227
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
;   LENGTH: 96
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
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;   OTHER INFORMATION: RNA aptamer
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(96)
;   OTHER INFORMATION: RNA aptamer
US-09-963-827B-23

  Query Match             53.3%;  Score 51.2;  DB 10;  Length 96;
  Best Local Similarity   70.8%;  Pred. No. 1.5e-09;
  Matches   68;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
              |||||||||||||||||||| |     || |     | |    |       || | ||
Db          1 GGGAGAGAGGAAGAGGGAUGGGAAAAUAGCCCCAGCGAGAUAAUACUUGGCCCCCGUACC 60

Qy         61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
              ||||||||||||||||||||||||||||||||||||
Db         61 ACCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96


RESULT 13
US-09-963-827B-11
; Sequence 11, Application US/09963827B
; Publication No. US20030175703A1
; GENERAL INFORMATION:
;  APPLICANT: Duke University
;  APPLICANT:  Sullenger, Bruce
;  APPLICANT:  Rusconi, Christopher
;  TITLE OF INVENTION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME
;  FILE REFERENCE: 180/124/2
;  CURRENT APPLICATION NUMBER: US/09/963,827B
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 60/235,654
;  PRIOR FILING DATE: 2000-09-26
;  NUMBER OF SEQ ID NOS: 227
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
;   LENGTH: 96
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: RNA aptamer
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (54)..(56)
;   OTHER INFORMATION: n=c, u or a
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(96)
;   OTHER INFORMATION: RNA aptamer
US-09-963-827B-11

  Query Match             52.9%;  Score 50.8;  DB 10;  Length 96;
  Best Local Similarity   69.8%;  Pred. No. 2.1e-09;
  Matches   67;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
              |||||||||||||||||||  |   || |   ||     |  | | |      |
Db          1 GGGAGAGAGGAAGAGGGAUGGGCUCAUCACAGGCGAAGUGAACAACACUACCGNCNAGUU 60

Qy         61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
              ||||||||||||||||||||||||||||||||||||
Db         61 ACCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96


RESULT 14
US-09-963-827B-6
; Sequence 6, Application US/09963827B
; Publication No. US20030175703A1
; GENERAL INFORMATION:
;  APPLICANT: Duke University
;  APPLICANT:  Sullenger, Bruce
;  APPLICANT:  Rusconi, Christopher
;  TITLE OF INVENTION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME
;  FILE REFERENCE: 180/124/2
;  CURRENT APPLICATION NUMBER: US/09/963,827B
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 60/235,654
;  PRIOR FILING DATE: 2000-09-26
;  NUMBER OF SEQ ID NOS: 227
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
;   LENGTH: 96
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: RNA aptamer
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(96)
;   OTHER INFORMATION: RNA aptamer
US-09-963-827B-6

  Query Match             51.7%;  Score 49.6;  DB 10;  Length 96;
  Best Local Similarity   69.8%;  Pred. No. 6e-09;
  Matches   67;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
              |||||||||||||||||||    ||  |  | |  || | ||   |
Db          1 GGGAGAGAGGAAGAGGGAUGGGCGAUAACCAACAUGGUGAUCCCAUUCAUCAUACCCUAC 60

Qy         61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
              ||||||||||||||||||||||||||||||||||||
Db         61 AACAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96


RESULT 15
US-09-963-827B-9
; Sequence 9, Application US/09963827B
; Publication No. US20030175703A1
; GENERAL INFORMATION:
;  APPLICANT: Duke University
;  APPLICANT:  Sullenger, Bruce
;  APPLICANT:  Rusconi, Christopher
;  TITLE OF INVENTION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME
;  FILE REFERENCE: 180/124/2
;  CURRENT APPLICATION NUMBER: US/09/963,827B
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 60/235,654
;  PRIOR FILING DATE: 2000-09-26
;  NUMBER OF SEQ ID NOS: 227
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
;   LENGTH: 96
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: RNA aptamer
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(96)
;   OTHER INFORMATION: RNA aptamer
US-09-963-827B-9

  Query Match             51.7%;  Score 49.6;  DB 10;  Length 96;
  Best Local Similarity   69.8%;  Pred. No. 6e-09;
  Matches   67;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
              |||||||||||||||||||          ||      ||    | | ||   | |   |
Db          1 GGGAGAGAGGAAGAGGGAUGGGACUAUAUUCGGAAUCUGGACUCCCACCUGCCUGCCCCA 60

Qy         61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
              ||||||||||||||||||||||||||||||||||||
Db         61 GACAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
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Search completed: April 9, 2004, 10:11:30
Job time : 1190.14 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 9, 2004, 03:18:00 ; Search time 306.071 Seconds
(without alignments)
200.961 Million cell updates/sec

Title: US-09-963-827B-3
Perfect score: 96
Sequence: 1 gggagagaggaagagggaug.....cgauaguacuggaucccccc 96

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1348483 seqs, 320354870 residues

Total number of hits satisfying chosen parameters: 1980062

Minimum DB seq length: 0
Maximum DB seq length: 200

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
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2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
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7: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	20.2	21.0	175	5	US-09-969-034-110	Sequence 110, App
	2	19.8	20.6	185	6	US-10-793-479-28742	Sequence 28742, A
c	3	19.8	20.6	187	6	US-10-793-479-13386	Sequence 13386, A
c	4	19.6	20.4	174	6	US-10-793-479-8881	Sequence 8881, Ap
c	5	19.4	20.2	155	6	US-10-803-180-1481	Sequence 1481, Ap
c	6	19.4	20.2	155	6	US-10-803-180-1490	Sequence 1490, Ap
c	7	19.4	20.2	156	6	US-10-803-180-1472	Sequence 1472, Ap
c	8	19.4	20.2	182	6	US-10-803-180-1488	Sequence 1488, Ap
c	9	19.4	20.2	182	6	US-10-803-180-1496	Sequence 1496, Ap
c	10	19.4	20.2	183	6	US-10-803-180-1479	Sequence 1479, Ap
c	11	19.2	20.0	51	6	US-10-785-782-6107	Sequence 6107, Ap
	12	19.2	20.0	160	6	US-10-793-479-10298	Sequence 10298, A
	13	19	19.8	51	6	US-10-785-782-8362	Sequence 8362, Ap
c	14	19	19.8	170	6	US-10-793-479-33426	Sequence 33426, A
c	15	19	19.8	194	6	US-10-803-180-1484	Sequence 1484, Ap
c	16	19	19.8	194	6	US-10-803-180-1493	Sequence 1493, Ap
c	17	19	19.8	195	6	US-10-803-180-1475	Sequence 1475, Ap
c	18	18.8	19.6	178	6	US-10-767-701-19121	Sequence 19121, A
c	19	18.6	19.4	51	6	US-10-785-782-23966	Sequence 23966, A
	20	18.6	19.4	101	6	US-10-708-204-7187	Sequence 7187, Ap
c	21	18.6	19.4	139	6	US-10-793-479-24132	Sequence 24132, A
	22	18.6	19.4	175	6	US-10-793-479-14465	Sequence 14465, A
c	23	18.6	19.4	183	6	US-10-793-479-16584	Sequence 16584, A
c	24	18.4	19.2	145	6	US-10-793-479-23541	Sequence 23541, A
	25	18.2	19.0	51	6	US-10-785-782-3679	Sequence 3679, Ap
	26	18.2	19.0	79	6	US-10-708-951-54485	Sequence 54485, A
	27	18	18.8	51	6	US-10-785-782-1281	Sequence 1281, Ap
c	28	18	18.8	81	6	US-10-708-951-58889	Sequence 58889, A
	29	18	18.8	129	6	US-10-793-479-24133	Sequence 24133, A
c	30	18	18.8	154	6	US-10-793-479-21521	Sequence 21521, A
	31	17.8	18.5	156	6	US-10-793-479-22764	Sequence 22764, A
c	32	17.8	18.5	158	6	US-10-793-479-19905	Sequence 19905, A
c	33	17.8	18.5	159	6	US-10-793-479-18305	Sequence 18305, A
	34	17.8	18.5	164	6	US-10-793-479-32124	Sequence 32124, A
c	35	17.8	18.5	165	6	US-10-793-479-26801	Sequence 26801, A
	36	17.8	18.5	196	6	US-10-775-972-317	Sequence 317, App
c	37	17.6	18.3	51	6	US-10-785-782-6108	Sequence 6108, Ap
	38	17.6	18.3	51	6	US-10-785-782-12949	Sequence 12949, A
	39	17.6	18.3	51	6	US-10-785-782-12951	Sequence 12951, A
	40	17.6	18.3	77	6	US-10-793-479-18123	Sequence 18123, A
	41	17.6	18.3	98	6	US-10-708-204-6705	Sequence 6705, Ap
	42	17.6	18.3	100	6	US-10-708-204-6783	Sequence 6783, Ap
	43	17.6	18.3	107	6	US-10-708-204-7061	Sequence 7061, Ap
	44	17.6	18.3	136	6	US-10-793-479-13949	Sequence 13949, A
c	45	17.6	18.3	138	6	US-10-793-479-22876	Sequence 22876, A

ALIGNMENTS

RESULT 1
US-09-969-034-110/c
; Sequence 110, Application US/09969034
; GENERAL INFORMATION:
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Astle, Jon H.
; APPLICANT: Carroll, Eddie III
; APPLICANT: Catino, Theodore J.
; APPLICANT: Dwivedi, Poornima
; APPLICANT: Molino, Gary A.
; APPLICANT: Thiagalingam, Arunthathi
; APPLICANT: Lewis, Marcia E.
; TITLE OF INVENTION: Nucleic Acid Sequences Differentially
; TITLE OF INVENTION: Expressed in Cancer Tissue
; FILE REFERENCE: 1657/1032
; CURRENT APPLICATION NUMBER: US/09/969,034
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/237,271
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 4494
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 175
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 12, 19, 35, 50, 51, 52, 67, 89, 90, 117, 118, 122, 129, 133,
; LOCATION: 144, 163
; OTHER INFORMATION: n = A,T,C or G
US-09-969-034-110

Query Match 21.0%; Score 20.2; DB 5; Length 175;
Best Local Similarity 41.2%; Pred. No. 2e+02;
Matches 33; Conservative 7; Mismatches 40; Indels 0; Gaps 0;

```
Qy         16 GGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGG 75
              | |: |||   |:  || |:|   | ||| | | |      |  ||  |:    ||||
Db        103 GTATTGGGGTCATNNCGAGTACGTCGGCCGCGCAAANGGTAAGGGCGAATTNNNCAGATA 44

Qy         76 UCGAUAGUACUGGAUCCCCC 95
              :| |:    |:||   || |
Db         43 TCCATCACNCTGGCGGCCGC 24
```

RESULT 2
US-10-793-479-28742
; Sequence 28742, Application US/10793479
; GENERAL INFORMATION:

```
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/10/793,479
;  CURRENT FILING DATE:  2004-03-03
;  PRIOR APPLICATION NUMBER: US/09/513,999
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 28742
;   LENGTH: 185
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-793-479-28742

  Query Match             20.6%;  Score 19.8;  DB 6;  Length 185;
  Best Local Similarity   38.1%;  Pred. No. 2.9e+02;
  Matches   24;  Conservative   12;  Mismatches   27;  Indels    0;  Gaps    0;

Qy         19 UGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCG 78
              :|| |||: :  | | :  : |:|  :| | |:     |||  :| :|||| || |:
Db         91 TGGTGACTCTTTCACTTCTTCCTGAATCACGATGGAAAAACCTTCTTAACCTTGATGTTA 150

Qy         79 AUA 81
              :|
Db        151 TTA 153


RESULT 3
US-10-793-479-13386/c
; Sequence 13386, Application US/10793479
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/10/793,479
;  CURRENT FILING DATE:  2004-03-03
;  PRIOR APPLICATION NUMBER: US/09/513,999
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 13386
;   LENGTH: 187
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-793-479-13386

  Query Match             20.6%;  Score 19.8;  DB 6;  Length 187;
  Best Local Similarity   49.1%;  Pred. No. 2.9e+02;
  Matches   27;  Conservative    6;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          8 AGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCU 62
              |||||| ||||:|   ||:      |   | ||:|||  |   ::| | | |||:
Db         70 AGGAAGGGGGATGCAAACTCACTGACACGAAGCTGCCATCTATTTCTGCAGCGCT 16


RESULT 4
US-10-793-479-8881/c
; Sequence 8881, Application US/10793479
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/10/793,479
;  CURRENT FILING DATE:  2004-03-03
;  PRIOR APPLICATION NUMBER: US/09/513,999
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 8881
;   LENGTH: 174
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 12
;   OTHER INFORMATION: s=g or c
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 13
;   OTHER INFORMATION: m=a or c
US-10-793-479-8881

  Query Match             20.4%;  Score 19.6;  DB 6;  Length 174;
  Best Local Similarity   57.1%;  Pred. No. 3.4e+02;
  Matches   24;  Conservative    4;  Mismatches   14;  Indels    0;  Gaps    0;

Qy         46 CCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGAUAGUACUG 87
              |||  ::|| |||| |:|| ||||    |  | | ||:|| |
Db         73 CCCTTTTCCAGAACACTCAAAACCTCATGAGCAAGAGTACAG 32


RESULT 5
US-10-803-180-1481/c
; Sequence 1481, Application US/10803180
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001511
;  CURRENT APPLICATION NUMBER: US/10/803,180
;  CURRENT FILING DATE:  2004-03-18
;  NUMBER OF SEQ ID NOS: 6676
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1481
;   LENGTH: 155
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-803-180-1481

  Query Match             20.2%;  Score 19.4;  DB 6;  Length 155;
  Best Local Similarity   55.6%;  Pred. No. 3.9e+02;
  Matches   25;  Conservative    4;  Mismatches   16;  Indels    0;  Gaps    0;

Qy         35 UAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGA 79
              :|| | :    ||||| :||  |  ||: | || |||||||  ||
Db         68 TAAAGGTTTAACCCCAATCCCAAGTGCTGAAAAACCAGAGGCTGA 24


RESULT 6
US-10-803-180-1490/c
; Sequence 1490, Application US/10803180
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001511
;  CURRENT APPLICATION NUMBER: US/10/803,180
;  CURRENT FILING DATE:  2004-03-18
;  NUMBER OF SEQ ID NOS: 6676
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1490
;   LENGTH: 155
;   TYPE: DNA
```

```
;   ORGANISM: Homo sapiens
US-10-803-180-1490

  Query Match             20.2%;  Score 19.4;  DB 6;  Length 155;
  Best Local Similarity   55.6%;  Pred. No. 3.9e+02;
  Matches   25;  Conservative    4;  Mismatches   16;  Indels    0;  Gaps    0;

Qy         35 UAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGA 79
              :|| | :    ||||| :||  |  ||: | || |||||||  ||
Db         68 TAAAGGTTTAACCCCAATCCCAAGTGCTGAAAAACCAGAGGCTGA 24


RESULT 7
US-10-803-180-1472/c
; Sequence 1472, Application US/10803180
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001511
;  CURRENT APPLICATION NUMBER: US/10/803,180
;  CURRENT FILING DATE:  2004-03-18
;  NUMBER OF SEQ ID NOS: 6676
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1472
;   LENGTH: 156
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-803-180-1472

  Query Match             20.2%;  Score 19.4;  DB 6;  Length 156;
  Best Local Similarity   55.6%;  Pred. No. 3.9e+02;
  Matches   25;  Conservative    4;  Mismatches   16;  Indels    0;  Gaps    0;

Qy         35 UAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGA 79
              :|| | :    ||||| :||  |  ||: | || |||||||  ||
Db         68 TAAAGGTTTAACCCCAATCCCAAGTGCTGAAAAACCAGAGGCTGA 24


RESULT 8
US-10-803-180-1488/c
; Sequence 1488, Application US/10803180
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001511
;  CURRENT APPLICATION NUMBER: US/10/803,180
;  CURRENT FILING DATE:  2004-03-18
;  NUMBER OF SEQ ID NOS: 6676
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1488
;   LENGTH: 182
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-803-180-1488

  Query Match             20.2%;  Score 19.4;  DB 6;  Length 182;
  Best Local Similarity   55.6%;  Pred. No. 4.1e+02;
  Matches   25;  Conservative    4;  Mismatches   16;  Indels    0;  Gaps    0;

Qy         35 UAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGA 79
              :|| | :    ||||| :||  |  ||: | || |||||||  ||
Db         95 TAAAGGTTTAACCCCAATCCCAAGTGCTGAAAAACCAGAGGCTGA 51


RESULT 9
US-10-803-180-1496/c
; Sequence 1496, Application US/10803180
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001511
;  CURRENT APPLICATION NUMBER: US/10/803,180
;  CURRENT FILING DATE:  2004-03-18
;  NUMBER OF SEQ ID NOS: 6676
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1496
;   LENGTH: 182
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-803-180-1496

  Query Match             20.2%;  Score 19.4;  DB 6;  Length 182;
  Best Local Similarity   55.6%;  Pred. No. 4.1e+02;
  Matches   25;  Conservative    4;  Mismatches   16;  Indels    0;  Gaps    0;

Qy         35 UAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGA 79
              :|| | :    ||||| :||  |  ||: | || |||||||  ||
Db         95 TAAAGGTTTAACCCCAATCCCAAGTGCTGAAAAACCAGAGGCTGA 51


RESULT 10
US-10-803-180-1479/c
; Sequence 1479, Application US/10803180
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001511
;  CURRENT APPLICATION NUMBER: US/10/803,180
;  CURRENT FILING DATE:  2004-03-18
;  NUMBER OF SEQ ID NOS: 6676
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1479
;   LENGTH: 183
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-803-180-1479

  Query Match             20.2%;  Score 19.4;  DB 6;  Length 183;
  Best Local Similarity   55.6%;  Pred. No. 4.1e+02;
  Matches   25;  Conservative    4;  Mismatches   16;  Indels    0;  Gaps    0;

Qy         35 UAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGA 79
              :|| | :    ||||| :||  |  ||: | || |||||||  ||
Db         95 TAAAGGTTTAACCCCAATCCCAAGTGCTGAAAAACCAGAGGCTGA 51


RESULT 11
US-10-785-782-6107/c
; Sequence 6107, Application US/10785782
; GENERAL INFORMATION:
;  APPLICANT: Leach, Martin
;  APPLICANT:  Shimkets, Richard A.
;  TITLE OF INVENTION: Nucleic Acids Containing Single Nucleotide Polymorphisms and Meti
;  TITLE OF INVENTION:  Use Thereof
;  FILE REFERENCE: 15966-611
;  CURRENT APPLICATION NUMBER: US/10/785,782
;  CURRENT FILING DATE:  2004-02-23
;  PRIOR APPLICATION NUMBER: US/09/755,374
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: 60/174962
;  PRIOR FILING DATE: 2000-01-07
;  NUMBER OF SEQ ID NOS: 28742
; SEQ ID NO 6107
;   LENGTH: 51
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (26)...(0)
;   OTHER INFORMATION: 1 of 2 allelic variants (6108 is other entry)
;   FEATURE:
;   NAME/KEY: misc_feature
```

```
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Accession number cg43986469
US-10-785-782-6107

  Query Match             20.0%;  Score 19.2;  DB 6;  Length 51;
  Best Local Similarity   52.5%;  Pred. No. 3.3e+02;
  Matches   21;  Conservative    6;  Mismatches   13;  Indels    0;  Gaps    0;

Qy         15 GGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCC 54
              | || ||||  : :|  | |: |: |:||| |||| : ||
Db         40 GTGAAGGGGTGTGTATGGAGTGATCCTGCCGCCCCCTCCC 1


RESULT 12
US-10-793-479-10298
; Sequence 10298, Application US/10793479
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/10/793,479
;  CURRENT FILING DATE:  2004-03-03
;  PRIOR APPLICATION NUMBER: US/09/513,999
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 10298
;   LENGTH: 160
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 41
;   OTHER INFORMATION: s=g or c
US-10-793-479-10298

  Query Match             20.0%;  Score 19.2;  DB 6;  Length 160;
  Best Local Similarity   53.6%;  Pred. No. 4.7e+02;
  Matches   30;  Conservative    3;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGG 56
              | | ||||||||||  |||:|||| |:    |  |    ||:|   |  ||  || |
Db         81 GAGTGAGAGGAAGGAGGATGGGGTCTGCCTCCTGAGTAGCTGGGACTACAGGCCCG 136


RESULT 13
US-10-785-782-8362
; Sequence 8362, Application US/10785782
; GENERAL INFORMATION:
;  APPLICANT: Leach, Martin
;  APPLICANT:  Shimkets, Richard A.
;  TITLE OF INVENTION: Nucleic Acids Containing Single Nucleotide Polymorphisms and Meth
;  TITLE OF INVENTION:  Use Thereof
;  FILE REFERENCE: 15966-611
;  CURRENT APPLICATION NUMBER: US/10/785,782
;  CURRENT FILING DATE:  2004-02-23
;  PRIOR APPLICATION NUMBER: US/09/755,374
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: 60/174962
;  PRIOR FILING DATE: 2000-01-07
;  NUMBER OF SEQ ID NOS: 28742
; SEQ ID NO 8362
;   LENGTH: 51
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (26)...(0)
;   OTHER INFORMATION: 2 of 2 allelic variants (8361 is other entry)
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Accession number cg43955877
US-10-785-782-8362

  Query Match             19.8%;  Score 19;  DB 6;  Length 51;
  Best Local Similarity   60.0%;  Pred. No. 3.9e+02;
  Matches   21;  Conservative    4;  Mismatches   10;  Indels    0;  Gaps    0;

Qy         61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCC 95
              |:   ||||| ||||:||| ||  |:|||:  | |
Db         10 CTATAAACCCTGAGGTCGAAAGCTCTGGATAGCTC 44


RESULT 14
US-10-793-479-33426/c
; Sequence 33426, Application US/10793479
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/10/793,479
;  CURRENT FILING DATE:  2004-03-03
;  PRIOR APPLICATION NUMBER: US/09/513,999
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 33426
;   LENGTH: 170
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-793-479-33426

  Query Match             19.8%;  Score 19;  DB 6;  Length 170;
  Best Local Similarity   52.9%;  Pred. No. 5.7e+02;
  Matches   27;  Conservative    4;  Mismatches   20;  Indels    0;  Gaps    0;

Qy         25 CUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGG 75
              |:|  | || :||: |  || ||| |: ||   || | ||  | | || ||
Db         87 CTAAGCAGCTTAATTCCTCCACCCTATACCCCTACTCCCAGCAGCAAGCGG 37


RESULT 15
US-10-803-180-1484/c
; Sequence 1484, Application US/10803180
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001511
;  CURRENT APPLICATION NUMBER: US/10/803,180
;  CURRENT FILING DATE:  2004-03-18
;  NUMBER OF SEQ ID NOS: 6676
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1484
;   LENGTH: 194
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-803-180-1484

  Query Match             19.8%;  Score 19;  DB 6;  Length 194;
  Best Local Similarity   55.6%;  Pred. No. 5.9e+02;
  Matches   25;  Conservative    4;  Mismatches   16;  Indels    0;  Gaps    0;

Qy         35 UAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGA 79
              :|| | :    ||||| :||  |  ||: | || |||||||  ||
Db        107 TAAAGGYTTAACCCCAATCCCAAGTGCTGAAAAACCAGAGGCTGA 63
```

Search completed: April 9, 2004, 09:18:37
Job time : 308.071 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 9, 2004, 02:50:24 ; Search time 2937.6 Seconds
(without alignments)
975.888 Million cell updates/sec

Title: US-09-963-827B-3
Perfect score: 96
Sequence: 1 gggagagaggaagagggaug.....cgauaguacuggaucccccc 96

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 3354136

Minimum DB seq length: 0
Maximum DB seq length: 200

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	27.6	28.8	139	28	AZ304985	AZ304985 1M0005C08
c	2	27.2	28.3	197	29	CE086809	CE086809 tigr-gss-
c	3	25.8	26.9	199	12	BG148573	BG148573 uu84a06.y
c	4	25.6	26.7	197	10	BE009953	BE009953 PM3-BN017
	5	25.4	26.5	175	10	BF000123	BF000123 7h18b01.x
	6	25.2	26.2	176	9	AA168469	AA168469 mr29b03.r
c	7	24	25.0	159	9	AV081297	AV081297 AV081297
	8	24	25.0	161	9	AV410806	AV410806 AV410806
c	9	23.8	24.8	200	29	CE002581	CE002581 tigr-gss-
c	10	23.4	24.4	117	29	BX893710	BX893710 Arabidops
	11	23.4	24.4	167	28	AZ603534	AZ603534 1M0422L20
	12	23.4	24.4	174	28	AQ934191	AQ934191 RPCI-23-2
c	13	23.4	24.4	181	9	AA414435	AA414435 vd08e10.s
c	14	23.4	24.4	190	12	BI082921	BI082921 602878291
	15	23.2	24.2	167	10	BB398492	BB398492 BB398492
c	16	23.2	24.2	190	28	AQ545235	AQ545235 CITBI-E1-
	17	23.2	24.2	192	13	BY317529	BY317529 BY317529
	18	23	24.0	155	14	CD150229	CD150229 ML1-0019T
c	19	23	24.0	155	14	CD150280	CD150280 ML1-0019T
c	20	23	24.0	179	28	AQ537838	AQ537838 RPCI-11-3
	21	23	24.0	187	12	BI013417	BI013417 QV3-ET017
	22	22.8	23.8	107	29	CG559758	CG559758 OST179226
c	23	22.8	23.8	166	13	BQ636379	BQ636379 hd08d09.y
c	24	22.8	23.8	187	9	AL035806	AL035806 DKFZp564B
	25	22.8	23.8	187	10	BF486945	BF486945 AT21535.5
	26	22.8	23.8	190	9	AV173481	AV173481 AV173481
c	27	22.8	23.8	192	14	CF641378	CF641378 D39_A05 F
c	28	22.8	23.8	193	14	CF060123	CF060123 QCS3d01.y
c	29	22.8	23.8	193	14	CF060356	CF060356 QCS6g09.y
c	30	22.8	23.8	197	14	CF081678	CF081678 QHL14A13.
	31	22.6	23.5	186	28	CC373112	CC373112 PUEFS27TD
c	32	22.6	23.5	189	9	AA737145	AA737145 nv91c03.r
	33	22.6	23.5	197	13	BY082301	BY082301 BY082301
c	34	22.6	23.5	199	9	AA860648	AA860648 aj82f01.s
	35	22.4	23.3	124	13	BQ976411	BQ976411 QHI21J10.
	36	22.4	23.3	127	10	BF364058	BF364058 QV0-NN102
	37	22.4	23.3	128	10	BF533294	BF533294 602073749
	38	22.4	23.3	133	14	N62783	N62783 yz82h02.s1
	39	22.4	23.3	144	10	AW797027	AW797027 QV1-UM003
	40	22.4	23.3	162	12	BI431277	BI431277 949066E11
c	41	22.4	23.3	163	13	BX098115	BX098115 BX098115
c	42	22.4	23.3	171	10	AW604870	AW604870 QV1-CT036
	43	22.4	23.3	173	9	AV068579	AV068579 AV068579
	44	22.4	23.3	185	10	BB044946	BB044946 BB044946
	45	22.4	23.3	186	29	CE443923	CE443923 tigr-gss-

ALIGNMENTS

RESULT 1
AZ304985
LOCUS AZ304985 139 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0005C08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0005C08 F, genomic survey sequence.
ACCESSION AZ304985
VERSION AZ304985.1 GI:10341550
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 139)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

```
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0005  row: C  column: 08
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 139.
FEATURES              Location/Qualifiers
     source           1. .139
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0005C08"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
ORIGIN

  Query Match             28.8%;  Score 27.6;  DB 28;  Length 139;
  Best Local Similarity   54.5%;  Pred. No. 2.1e+02;
  Matches   36;  Conservative    6;  Mismatches   24;  Indels    0;  Gaps    0;

Qy         10 GAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACC 69
              | ||||||    ||   |:|||   :||: |:||  |||||::| |  | || ||  ||
Db         22 GGAGAGGGTACCGGGTCATACCTACTAATACTGCTACCCCATTCTGCCATGCCCAGCACT 81

Qy         70 CAGAGG 75
                ||||
Db         82 GGGAGG 87


RESULT 2
CE086809/c
LOCUS       CE086809                197 bp    DNA     linear   GSS 24-SEP-2003
DEFINITION  tigr-gss-dog-17000359035311 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION   CE086809
VERSION     CE086809.1  GI:35153655
KEYWORDS    GSS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 197)
  AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
  TITLE     The dog genome: survey sequencing and comparative analysis
  JOURNAL   Science 301 (5641), 1898-1903 (2003)
  MEDLINE   22875432
   PUBMED   14512627
COMMENT     Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirknes@tigr.org
            Class: shotgun.
FEATURES              Location/Qualifiers
     source           1. .197
                      /organism="Canis familiaris"
                      /mol_type="genomic DNA"
                      /strain="Standard Poodle"
                      /db_xref="taxon:9615"
                      /clone_lib="Dog Library"
                      /note="Site_1: BstXI; Libraries were prepared from
                      peripheral blood"
ORIGIN

  Query Match             28.3%;  Score 27.2;  DB 29;  Length 197;
  Best Local Similarity   50.0%;  Pred. No. 3e+02;
  Matches   40;  Conservative    7;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
              | |||||||| ||||  |  || ||    || ||     |: ||:  ||| : |     |
Db        136 GAGAGAGAGGCAGAGACACAGGCACCCCCCCCCGCCCACCTCCCTTTCCACTACCCCTTG 77

Qy         61 CUCAUAACCCAGAGGUCGAU 80
                :||:  |||||| : | :
Db         76 TTCATTTCCCAGAGTTAGGT 57


RESULT 3
BG148573/c
LOCUS       BG148573                199 bp    mRNA    linear   EST 01-FEB-2001
DEFINITION  uu84a06.y1 Soares_mouse_NMGB_bcell Mus musculus cDNA clone
            IMAGE:3382955 5' similar to SW:PRI2_MOUSE P33610 DNA PRIMASE LARGE
            SUBUNIT ;, mRNA sequence.
ACCESSION   BG148573
VERSION     BG148573.1  GI:12651995
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 199)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:1087951
            Trace considered overall poor quality
            Seq primer: -40RP from Gibco
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .199
                      /organism="Mus musculus"
                      /mol_type="mRNA"
                      /db_xref="taxon:10090"
                      /clone="IMAGE:3382955"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="Soares_mouse_NMGB_bcell"
                      /note="Organ: germinal B-cell; Vector: pT7T3D-Pac
                      (Pharmacia) with a modified polylinker; Site_1: Not I;
                      Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                      oligo(dT) primer [5'
                      TGTTACCAATCTGAAGTGGGAGCGGCCGCCTGGTTTTTTTTTTTTTTTTTTTTTTT
                      T 3']; double-stranded cDNA was ligated to Eco RI
                      adaptors (Pharmacia), digested with Not I and cloned into
                      the Not I and Eco RI sites of  the modified pT7T3 vector.
                      Library is normalized; constructed by Bento Soares and
                      M.Fatima Bonaldo."
```

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ORIGIN

  Query Match            26.9%;  Score 25.8;  DB 12;  Length 199;
  Best Local Similarity  41.9%;  Pred. No. 8.4e+02;
  Matches   39;  Conservative   12;  Mismatches   42;  Indels    0;  Gaps    0;

Qy          1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
              |||  |||| |  ||  | | ||||  :|    |: |  |:|||:||   ::   |   |
Db        101 GGGGCAGAGCATCAGCAAAGAGGACCTTATAATGTGACTCTGCCTCCAACTTGATGCCTG 42

Qy         61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCC 93
              :  :    ||||||: | :  :|    |:|||
Db         41 TTAGTGTTGCAGAGGTAGCTGCTATGATATCCC 9


RESULT 4
BE009953/c
LOCUS       BE009953                197 bp    mRNA    linear   EST 05-JUN-2000
DEFINITION  PM3-BN0174-130500-007-d04 BN0174 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE009953
VERSION     BE009953.1  GI:8270186
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 197)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=PM3-BN0174-130
            500-007-d04&t3=2000-05-13&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 56
            High quality sequence stop: 197.
FEATURES             Location/Qualifiers
     source          1. .197
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="BN0174"
                     /note="Organ: breast_normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

  Query Match            26.7%;  Score 25.6;  DB 10;  Length 197;
  Best Local Similarity  55.4%;  Pred. No. 9.7e+02;
  Matches   31;  Conservative    6;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGG 56
              | |||||||| ||| |||:  ||| : :||| |   | ||: |   | | ::|| |
Db        119 GTGAGAGAGGGAGAAGGATCTGGAGTCTACCTCCAGAAGCTCCTGGCTCCTTCCTG 64


RESULT 5
BF000123
LOCUS       BF000123                175 bp    mRNA    linear   EST 06-OCT-2000
DEFINITION  7h18b01.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3316297 3'
            similar to TR:Q9W6S3 Q9W6S3 SAPK INTERACTING PROTEIN. ;, mRNA
            sequence.
ACCESSION   BF000123
VERSION     BF000123.1  GI:10700398
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 175)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
            M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov
            Trace considered overall poor quality
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .175
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3316297"
                     /tissue_type="colon tumor, RER+"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Co16"
                     /note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Plasmid DNA from the normalized library NCI_CGAP_Co10 was
                     prepared, and ss circles were made in vitro. Following HAP
                     purification, this DNA was used as tracer in a subtractive
                     hybridization reaction. The driver was PCR-amplified cDNAs
                     from a pool of 5,000 clones made from the same library
                     (cloneIDs 1057416-1061255, and 1144584-1145351).
                     Subtraction by Bento Soares and M. Fatima Bonaldo.  "
ORIGIN

  Query Match            26.5%;  Score 25.4;  DB 10;  Length 175;
  Best Local Similarity  52.9%;  Pred. No. 1.1e+03;
  Matches   27;  Conservative    8;  Mismatches   16;  Indels    0;  Gaps    0;

Qy         30 CCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGAU 80
              ||| | | :||:|||:| | |::|| |   ||:  :||||| ||   | |:
Db         83 CCGGGCAGTGCTGCCTCTCAATTCCAGCCTGCTGTTAACCCTGATCACTAT 133


RESULT 6
AA168469
LOCUS       AA168469                176 bp    mRNA    linear   EST 16-FEB-1997
DEFINITION  mr29b03.r1 Soares mouse 3NbMS Mus musculus cDNA clone IMAGE:598829
            5', mRNA sequence.
ACCESSION   AA168469
VERSION     AA168469.1  GI:1746690
KEYWORDS    EST.
```

```
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 176)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:364261
            Seq primer: -28M13 rev2 from Amersham.
FEATURES             Location/Qualifiers
     source          1. .176
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:598829"
                     /sex="male"
                     /tissue_type="Spleen"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /clone_lib="Soares mouse 3NbMS"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGCTGTTTTTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. RNA
                     provided by Dr. Bertrand Jordan. Library went through
                     three rounds of normalization, and was constructed by
                     Bento Soares and M.Fatima Bonaldo."
ORIGIN

  Query Match             26.2%;  Score 25.2;  DB 9;  Length 176;
  Best Local Similarity   44.9%;  Pred. No. 1.3e+03;
  Matches   35;  Conservative   10;  Mismatches   33;  Indels    0;  Gaps    0;

Qy         17 GAUGGGGACUAUAACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGU 76
              ||:| ||| : :|| || :  : |   |: ||| : || |  | |:| :|  |  ||||
Db         21 GATGAGGAATGTACTGCTTTGTTCATGCTGCCCCTACCAGGCCACTCCTACTCATGAGGA 80

Qy         77 CGAUAGUACUGGAUCCCC 94
              ||   |  |    :||||
Db         81 CGGAGGGCCACCCTCCCC 98


RESULT 7
AV081297/c
LOCUS       AV081297                159 bp    mRNA    linear   EST 25-JUN-1999
DEFINITION  AV081297 Mus musculus stomach C57BL/6J adult Mus musculus cDNA
            clone 2210418F19, mRNA sequence.
ACCESSION   AV081297
VERSION     AV081297.1  GI:5212745
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 159)
  AUTHORS   Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
            Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T.,
            Hara,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M.,
            Kawai,J., Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H.,
            Owa,C., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y.,
            Sugahara,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y.,
            Tominaga,N., Watanabe,S., Yagame,M., Yamamura,T., Yokota,T.,
            Yoshino,M., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Chie Owa
            Genome Science Laboratory
            RIKEN
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: 81-298-36-9145
            Fax: 81-298-36-9098
            Email: genome-res@rtc.riken.go.jp
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length cDNA
            (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
            Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
            Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .159
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="2210418F19"
                     /sex="male"
                     /tissue_type="stomach"
                     /dev_stage="adult"
                     /clone_lib="Mus musculus stomach C57BL/6J adult"
ORIGIN

  Query Match             25.0%;  Score 24;  DB 9;  Length 159;
  Best Local Similarity   48.5%;  Pred. No. 3e+03;
  Matches   32;  Conservative    7;  Mismatches   27;  Indels    0;  Gaps    0;

Qy          4 AGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUC 63
              | |||| ||||| ||  ||| |:|    |||  |:  :  | |||| :: |      |:|
Db         66 AAAGAGCAAGAGAGAAAGGGCCTAGCATGCGAGATCNTCGCCCCCCCTTTCTNCTTACTC 7

Qy         64 AUAACC 69
              |: | |
Db          6 ATCAAC 1


RESULT 8
AV410806
LOCUS       AV410806                161 bp    mRNA    linear   EST 28-JUL-2003
DEFINITION  AV410806 Lotus japonicus young plants (two-week old) Lotus
            corniculatus var. japonicus cDNA clone MWL078d06_r 5', mRNA
            sequence.
ACCESSION   AV410806
VERSION     AV410806.1  GI:7723660
KEYWORDS    EST.
SOURCE      Lotus corniculatus var. japonicus (Lotus japonicus)
  ORGANISM  Lotus corniculatus var. japonicus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
            Lotus.
REFERENCE   1  (bases 1 to 161)
  AUTHORS   Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
  TITLE     Generation of 7137 non-redundant expressed sequence tags from a
            legume, Lotus japonicus
  JOURNAL   DNA Res. 7 (2), 127-130 (2000)
  MEDLINE   20277479
   PUBMED   10819328
COMMENT     Contact: Yasukazu Nakamura
```

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           The First Laboratory for Plant Gene Research
           Kazusa DNA Research Institute
           Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
           Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES             Location/Qualifiers
     source          1. .161
                     /organism="Lotus corniculatus var. japonicus"
                     /mol_type="mRNA"
                     /isolate="Miyakojima MG-20"
                     /db_xref="taxon:34305"
                     /clone="MWL078d06_r"
                     /dev_stage="young plants (two-week old)"
                     /clone_lib="Lotus japonicus young plants (two-week old)"
                     /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                     XhoI; synonym: Lotus japonicus"
ORIGIN

  Query Match             25.0%;  Score 24;  DB 9;  Length 161;
  Best Local Similarity   50.0%;  Pred. No. 3e+03;
  Matches   32;  Conservative    7;  Mismatches   25;  Indels    0;  Gaps    0;

Qy         18 AUGGGGACUAUACCGCGUAAUGCUGCCUCCCCCAUUCCGGAACGCUCAUAACCCAGAGGUC 77
              |:|||   :  |||  |:||:|  | | || | ::|||   | |:|| |||   | ||
Db         94 ATGGGTCGTCCACCCAGTAATGGAGGCCCCGCCTTCCGCTTCACTCAGAACGAGGTGGCA 153

Qy         78 GAUA 81
              || |
Db        154 GAAA 157


RESULT 9
CE002581/c
LOCUS       CE002581                200 bp    DNA     linear   GSS 24-SEP-2003
DEFINITION  tigr-gss-dog-17000320893726 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION   CE002581
VERSION     CE002581.1  GI:34999116
KEYWORDS    GSS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 200)
  AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
  TITLE     The dog genome: survey sequencing and comparative analysis
  JOURNAL   Science 301 (5641), 1898-1903 (2003)
  MEDLINE   22875432
   PUBMED   14512627
COMMENT     Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirknes@tigr.org
            Class: shotgun.
FEATURES             Location/Qualifiers
     source          1. .200
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /strain="Standard Poodle"
                     /db_xref="taxon:9615"
                     /clone_lib="Dog Library"
                     /note="Site_1: BstXI; Libraries were prepared from
                     peripheral blood"
ORIGIN

  Query Match             24.8%;  Score 23.8;  DB 29;  Length 200;
  Best Local Similarity   53.7%;  Pred. No. 3.6e+03;
  Matches   36;  Conservative    4;  Mismatches   27;  Indels    0;  Gaps    0;

Qy          2 GGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGC 61
              || |||||||||  || | |||       || |  : | || | |:|||||  :  | |  |
Db        102 GGGGAGAGGAAATGGAAGGGGAGAGGGACAGTTTCAAGCAGACTCCCCACTAAGCACGGA 43

Qy         62 UCAUAAC 68
              :|  |||
Db         42 TCTCAAC 36


RESULT 10
BX893710/c
LOCUS       BX893710                117 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence GK-649H06-023273,
            genomic survey sequence.
ACCESSION   BX893710
VERSION     BX893710.1  GI:39926205
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
            and Weisshaar,B.
  TITLE     A pipeline for automated high-throughput generation of FSTs
            (flanking sequence tags) from Arabidopsis thaliana T-DNA
            transformed lines
  JOURNAL   Unpublished
REFERENCE   2
  AUTHORS   Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
  TITLE     A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
            for flanking sequence tag based reverse genetics
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 117)
  AUTHORS   Strizhov,N., Li,Y., Rosso,M. and Weisshaar,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-DEC-2003) Weisshaar B., Max-Planck-Institut fuer
            Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT     This sequence is recovered from the left border of the T-DNA. It
            indicates an insertion close to or within gene At1g06940. The
            sequences are generated at the MPI for Plant Breeding Research in
            the context of the GABI-Kat project. GABI-Kat is part of the German
            Plant Genomics program designated 'GABI'. Information on line
            availability can be found at:
            http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES             Location/Qualifiers
     source          1. .117
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="GK-649H06-023273"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                     /note="PCR was performed on DNA from Arabidopsis thaliana
                     plants (T1) which were transformed with the T-DNA from
                     vector pAC161. The lines contain one or more T-DNA
                     insertions. The DNA fragment(s) resulting from the PCR
                     were directly sequenced to determine the genomic sequence
                     flanking the insertion. Sequences displaying significant
                     similarity to the A. thalaina nuclear genome sequence were
                     processed for submission. T-DNA derived sequences were
                     removed"
ORIGIN

  Query Match             24.4%;  Score 23.4;  DB 29;  Length 117;
  Best Local Similarity   52.0%;  Pred. No. 4.4e+03;
  Matches   39;  Conservative    3;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
              ||||| | || |||| |   |||   | ||  |  ||:|  || : || |  | |   |
Db        112 GGGAGGGGGGCAGAGCGGCTGGGCGCAAACGTCCAAATGGGGCNTNCCAACCCAGTGCCT 53
```

```
Qy          61 CUCAUAACCCAGAGG 75
               |:||  |    ||||
Db          52 CTCACTATAGGGAGG 38


RESULT 11
AZ603534
LOCUS       AZ603534                167 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0422L20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0422L20 R, genomic survey sequence.
ACCESSION   AZ603534
VERSION     AZ603534.1  GI:11725724
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 167)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0422  row: L  column: 20
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 167.
FEATURES             Location/Qualifiers
     source          1. .167
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0422L20"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match            24.4%;  Score 23.4;  DB 28;  Length 167;
  Best Local Similarity  49.2%;  Pred. No. 4.7e+03;
  Matches   32;  Conservative    7;  Mismatches   26;  Indels    0;  Gaps    0;

Qy           1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
               | ||||||| |||| ||  | |    :||| |   |:| :  |:| |   :|| |  |
Db         100 GAGAGAGAGAGAGAGAGAGCGCACGTACCACAGGATGTTATCTCACTTGTCCTCAGTG 159

Qy          61 CUCAU 65
               |:||:
Db         160 CTCAT 164


RESULT 12
AQ934191
LOCUS       AQ934191                174 bp    DNA     linear   GSS 21-DEC-1999
DEFINITION  RPCI-23-282P11.TV RPCI-23 Mus musculus genomic clone
            RPCI-23-282P11, genomic survey sequence.
ACCESSION   AQ934191
VERSION     AQ934191.1  GI:6623205
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 174)
  AUTHORS   Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,
            Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de
            Jong,P. and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-23
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: RPCI-23-282P11.TJ
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-23. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
            or from Resea ch Genetics (info@resgen.com). BAC end page:
            http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 282  row: P  column: 11
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .174
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="RPCI-23-282P11"
                     /sex="Female"
                     /lab_host="DH10B"
                     /clone_lib="RPCI-23"
                     /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
                     EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
                     brain genomic DNA was isolated and  partially digested
                     with a combination of EcoRI and EcoRI Methylase.   Size
                     selected DNA was cloned into the pBACe3.6 vector at the
                     EcoRI  sites.  The ligation products were transformed into
                     DH10B  electrocompetent cells (BRL Life Technologies).   "
ORIGIN

  Query Match            24.4%;  Score 23.4;  DB 28;  Length 174;
  Best Local Similarity  54.4%;  Pred. No. 4.7e+03;
  Matches   31;  Conservative    5;  Mismatches   21;  Indels    0;  Gaps    0;

Qy           1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGA 57
               | |  |||| | || |||:|||||  |:|||  | ||:|    |    | ::|| ||
Db          73 GTGTTAGAGCATGATGGATGGGGAACATACCTGGGAATGAGAGCAAATCCTTCCTGA 129


RESULT 13
```

```
AA414435/c
LOCUS       AA414435                181 bp    mRNA    linear   EST 04-AUG-1997
DEFINITION  vd08e10.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone
            IMAGE:791946 5' similar to TR:G1136422 G1136422 KIAA0181 PROTEIN ;,
            mRNA sequence.
ACCESSION   AA414435
VERSION     AA414435.1  GI:2074572
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 181)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:476354
            Possible reversed clone: similarity on wrong strand
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 178.
FEATURES             Location/Qualifiers
     source          1. .181
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J x DBA/2J F1"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:791946"
                     /tissue_type="embryo"
                     /dev_stage="2-cell"
                     /lab_host="DH10B"
                     /clone_lib="Knowles Solter mouse 2 cell"
                     /note="Organ: embryo; Vector: pBluescribe (modified);
                     Site_1: MluI; Site_2: SalI; Cloned unidirectionally from
                     mRNA prepared from 13,500 2-cell stage embryos. Primer:
                     SalI(dT): 5'-CGGTCGACCGTCGACCGTTTTTTTTTTTTTTT-3'.  cDNAs
                     were cloned into the MluI/SalI sites of a modified
                     pBluescribe vector using commercial linkers (NEB).
                     Average insert size:  1.2 kb."
ORIGIN

  Query Match             24.4%;  Score 23.4;  DB 9;  Length 181;
  Best Local Similarity   55.1%;  Pred. No. 4.8e+03;
  Matches   27;  Conservative    6;  Mismatches   16;  Indels    0;  Gaps    0;

Qy         32 GCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGAU 80
              | | ||: |:|||:|| | :  |||||    || |  ||| |||:| |:
Db         60 GGGAAATCCTGCCTCCACCTAACGGAATTTCCAGATGCCACAGGTCCAT 12


RESULT 14
BI082921/c
LOCUS       BI082921                190 bp    mRNA    linear   EST 20-JUN-2001
DEFINITION  602878291F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5009686 5',
            mRNA sequence.
ACCESSION   BI082921
VERSION     BI082921.1  GI:14501251
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 190)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11056  row: f  column: 23
            High quality sequence stop: 94.
FEATURES             Location/Qualifiers
     source          1. .190
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="FVB/N-3"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5009686"
                     /tissue_type="tumor, biopsy sample"
                     /dev_stage="5 months"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Mam2"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigator
                     providing samples: Gilbert Smith, NIH"
ORIGIN

  Query Match             24.4%;  Score 23.4;  DB 12;  Length 190;
  Best Local Similarity   67.6%;  Pred. No. 4.8e+03;
  Matches   23;  Conservative    4;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          4 AGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAA 37
              |||||||||||||||: | |  : :|| || :||
Db        117 AGAGAGGAAGAGGGATTGTGTNTCTACAGCCTAA 84


RESULT 15
BB398492
LOCUS       BB398492                167 bp    mRNA    linear   EST 15-JUL-2000
DEFINITION  BB398492 RIKEN full-length enriched, ES cells Mus musculus cDNA
            clone C330008G22 3' similar to AF087680 Mus musculus valyl-tRNA
            synthetase (G7a) mRNA, mRNA sequence.
ACCESSION   BB398492
VERSION     BB398492.1  GI:9217888
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 167)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T.,
            Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C.,
            Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,
            Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K.,
            Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A.,
            Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A.,
            Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A.,
            Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
```

Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA.. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
source 1. .167
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="C330008G22"
/cell_type="ES cells"
/lab_host="SOLR"
/clone_lib="RIKEN full-length enriched, ES cells"
/note="Site_1: XhoI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0 and subtraction to Rot = 25.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']."

ORIGIN

Query Match 24.2%; Score 23.2; DB 10; Length 167;
Best Local Similarity 44.6%; Pred. No. 5.4e+03;
Matches 41; Conservative 8; Mismatches 43; Indels 0; Gaps 0;

```
Qy          2 GGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGC 61
              ||   | ||| ||||     |  |: : ||     |:||:|   ||||        ||| |
Db         50 GGCAGGTGGATGAGGCCATCGCCCTTTTCCAGAAGATGCTGTGACCCCCCATTCCAACCC 109

Qy         62 UCAUAACCCAGAGGUCGAUAGUACUGGAUCCC 93
                :||   ||||| | :| |:      |||: ||
Db        110 TCACCCCCCAGTGTTCCATCTACAGGGATGCC 141
```

Search completed: April 9, 2004, 06:03:50
Job time : 2945.1 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 9, 2004, 01:42:24 ; Search time 283.067 Seconds
(without alignments)
5206.064 Million cell updates/sec

Title: US-09-963-827B-70
Perfect score: 34
Sequence: 1 auggggacuauaccgcguaaugcugccuccccau 34

Scoring table: IDENTITY_NUC
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	17.2	50.6	77	6	AX902260	AX902260 Sequence
2	17.2	50.6	77	6	BD037793	BD037793 Sequence
3	17.2	50.6	115	6	AR422268	AR422268 Sequence
4	17.2	50.6	115	6	BD117821	BD117821 EST and e
5	17.2	50.6	196	6	BD275880	BD275880 COMPOUNDS
6	17.2	50.6	196	6	AR220665	AR220665 Sequence
7	17.2	50.6	196	6	AR255659	AR255659 Sequence
8	17.2	50.6	196	6	AR281229	AR281229 Sequence
9	17.2	50.6	196	6	AX365924	AX365924 Sequence
10	17	50.0	104	10	S42430	S42430 T cell rece
11	17	50.0	123	10	MMU26786	U26786 Mus musculu
12	17	50.0	135	10	AY089788	AY089788 Mus muscu
13	17	50.0	157	10	AF012183	AF012183 Mus muscu
14	17	50.0	176	11	AU048750	AU048750 Rattus no
15	17	50.0	186	8	PCH543747	AJ543747 Phaneroch
16	16.8	49.4	188	11	HUMSWX854	L24891 Human chrom
c 17	16.2	47.6	161	1	AY040741	AY040741 Unculture
18	16	47.1	85	9	HUMLBP31	D28372 Homo sapien
c 19	16	47.1	113	5	AMTMHA2A	M81089 Ambystoma m
c 20	16	47.1	127	4	AF006569	AF006569 Sus scrof
c 21	16	47.1	189	1	CLI536093	AJ536093 Unculture
22	15.8	46.5	94	9	F193462S03	AF193464 Pan trogl
c 23	15.8	46.5	160	1	AY013620	AY013620 Unculture
c 24	15.8	46.5	167	1	AF509475	AF509475 Bacterium
c 25	15.8	46.5	180	9	HAJ9270	AJ229270 Homo sapi
c 26	15.6	45.9	141	6	AX913011	AX913011 Sequence
c 27	15.6	45.9	141	6	BD048544	BD048544 Sequence
28	15.6	45.9	159	9	F193462S14	AF193475 Pan trogl
c 29	15.4	45.3	38	6	AR286969	AR286969 Sequence
c 30	15.4	45.3	38	6	AR398959	AR398959 Sequence
c 31	15.4	45.3	64	6	AX202684	AX202684 Sequence
32	15.4	45.3	78	10	AF096388	AF096388 Mus muscu
33	15.4	45.3	78	10	AF096389	AF096389 Mus muscu
34	15.4	45.3	87	10	AF096378	AF096378 Mus muscu
35	15.4	45.3	123	10	AY089787	AY089787 Mus muscu
36	15.4	45.3	147	6	AR173337	AR173337 Sequence
37	15.4	45.3	151	10	HAMADBL1	M12409 Adenovirus
c 38	15.4	45.3	160	9	HSU32641	U32641 Human ret/P
c 39	15.4	45.3	163	1	AF528054	AF528054 Haemophil
40	15.4	45.3	164	10	MMMARK001	X58257 Mouse monon
c 41	15.4	45.3	183	11	HUMUT452A	L29983 Human STS U
42	15.4	45.3	190	1	ASP493433	AJ493433 Agrobacte
43	15.4	45.3	190	1	NSP493434	AJ493434 Neisseria
44	15.4	45.3	196	9	HS170E10R	Z57295 H.sapiens C
c 45	15.4	45.3	198	11	G26726	G26726 human STS S

ALIGNMENTS

RESULT 1
AX902260
LOCUS AX902260 77 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 18123 from Patent EP1033401.
ACCESSION AX902260
VERSION AX902260.1 GI:40057217
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 18123 06-SEP-2000;

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           Genset (FR)
FEATURES             Location/Qualifiers
     source          1. .77
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
ORIGIN

  Query Match             50.6%;  Score 17.2;  DB 6;  Length 77;
  Best Local Similarity   56.7%;  Pred. No. 1.2e+05;
  Matches   17;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          2 UGGGGACUAUACCGCGUAAUGCUGCCUCCC 31
              :||| ||:|:  |  | ||  |:|||:|||
Db          4 TGGGAACTATGTCAGGAAAACCTGCCTCCC 33


RESULT 2
BD037793
LOCUS       BD037793                 77 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Sequence tag and encoded human protein.
ACCESSION   BD037793
VERSION     BD037793.1  GI:22579535
KEYWORDS    JP 2001269182-A/14039.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 77)
  AUTHORS   Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
  TITLE     Sequence tag and encoded human protein
  JOURNAL   Patent: JP 2001269182-A 14039 02-OCT-2001;
            GENSET
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001269182-A/14039
            PD   02-OCT-2001
            PF   24-FEB-2000 JP 2000118773
            PR   26-FEB-1999 US    60/122487
            PI   JEAN BAPUTIST DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES
            PI   JORDAN
            PC   C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC
             C12N5/10,
            PC   C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC
              G06F15/40
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            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             50.6%;  Score 17.2;  DB 6;  Length 77;
  Best Local Similarity   56.7%;  Pred. No. 1.2e+05;
  Matches   17;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          2 UGGGGACUAUACCGCGUAAUGCUGCCUCCC 31
              :||| ||:|:  |  | ||  |:|||:|||
Db          4 TGGGAACTATGTCAGGAAAACCTGCCTCCC 33


RESULT 3
AR422268
LOCUS       AR422268                115 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 13765 from patent US 6639063.
ACCESSION   AR422268
VERSION     AR422268.1  GI:40177378
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 115)
  AUTHORS   Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
  TITLE     EST's and encoded human proteins
  JOURNAL   Patent: US 6639063-A 13765 28-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .115
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             50.6%;  Score 17.2;  DB 6;  Length 115;
  Best Local Similarity   56.7%;  Pred. No. 1e+05;
  Matches   17;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          3 GGGGACUAUACCGCGUAAUGCUGCCUCCCC 32
              || || :  || || : |:||: ||:||||
Db         63 GGAGATTGGACGGCCTGATGCTCCCTCCCC 92


RESULT 4
BD117821
LOCUS       BD117821                115 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  EST and encoded human protein.
ACCESSION   BD117821
VERSION     BD117821.1  GI:23212725
KEYWORDS    JP 2002010789-A/9898.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 115)
  AUTHORS   Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.
  TITLE     EST and encoded human protein
  JOURNAL   Patent: JP 2002010789-A 9898 15-JAN-2002;
            GENSET CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002010789-A/9898
            PD   15-JAN-2002
            PF   07-AUG-2000 JP 2000280989
            PR   05-AUG-1999 US    60/147499
            PI   JEAN BAPUTIST DUMAS MILNE EDWARDS,SEVELIN JOBERT,JEAN EVE  PI
             GIORDANO
            PC   C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19, PC
             C12N1/21,
            PC   C12N5/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5/00, PC
            C12N15/00
            CC   EST and encoded human protein
            FH   Key             Location/Qualifiers
            FT   source          1. .115
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .115
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             50.6%;  Score 17.2;  DB 6;  Length 115;
  Best Local Similarity   56.7%;  Pred. No. 1e+05;
  Matches   17;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          3 GGGGACUAUACCGCGUAAUGCUGCCUCCCC 32
              || || :  || || : |:||: ||:||||
Db         63 GGAGATTGGACGGCCTGATGCTCCCTCCCC 92


RESULT 5
BD275880
LOCUS       BD275880                196 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  COMPOUNDS AND METHODS FOR THERAPY AND DIAGNOSIS OF LUNG CANCER.
ACCESSION   BD275880
VERSION     BD275880.1  GI:33085648
KEYWORDS    JP 2002543769-A/274.
SOURCE      unidentified
```

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  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 196)
  AUTHORS   Wang,T. and Van,R.
  TITLE     COMPOUNDS AND METHODS FOR THERAPY AND DIAGNOSIS OF LUNG CANCER
  JOURNAL   Patent: JP 2002543769-A 274 24-DEC-2002;
            Corixa Corporation et al
COMMENT     OS   Homo sapien
            PN   JP 2002543769-A/274
            PD   24-DEC-2002
            PF   03-APR-2000 JP 2000611554
            PR   22-FEB-2000 US    09/510376,10-JAN-2000 US    09/480884, PR
            02-APR-1999 US    09/285479,30-DEC-1999 US    09/476496, PR
            17-DEC-1999 US    09/466396
            PI   tongtong wang,rikn van
            CC
            FH   Key             Location/Qualifiers.
FEATURES            Location/Qualifiers
     source         1. .196
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"
ORIGIN

  Query Match             50.6%;  Score 17.2;  DB 6;  Length 196;
  Best Local Similarity   56.7%;  Pred. No. 8.2e+04;
  Matches   17;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          3 GGGGACUAUACCGCGUAAUGCUGCCUCCCC 32
              || ||  :  || ||  : |:||: ||:|||| 
Db        104 GGAGATTGGACGGCCTGATGCTCCCTCCCC 133


RESULT 6
AR220665
LOCUS       AR220665                196 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 317 from patent US 6426072.
ACCESSION   AR220665
VERSION     AR220665.1  GI:23327446
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 196)
  AUTHORS   Wang,T., Fan,L., Kalos,M.D., Bangur,C.S., Hosken,N.A., Fanger,G.R.,
            Li,S.X., Wang,A., Skeiky,Y.A.W., Henderson,R.A. and McNeill,P.D.
  TITLE     Compositions and methods for the therapy and diagnosis of lung
            cancer
  JOURNAL   Patent: US 6426072-A 317 30-JUL-2002;
FEATURES            Location/Qualifiers
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ORIGIN

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  Best Local Similarity   56.7%;  Pred. No. 8.2e+04;
  Matches   17;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          3 GGGGACUAUACCGCGUAAUGCUGCCUCCCC 32
              || ||  :  || ||  : |:||: ||:|||| 
Db        104 GGAGATTGGACGGCCTGATGCTCCCTCCCC 133


RESULT 7
AR255659
LOCUS       AR255659                196 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 317 from patent US 6482597.
ACCESSION   AR255659
VERSION     AR255659.1  GI:27304708
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 196)
  AUTHORS   Wang,T., Hosken,N.A., Kalos,M.D., Fanger,G.R. and Fan,L.
  TITLE     Compounds and methods for therapy and diagnosis of lung cancer
  JOURNAL   Patent: US 6482597-A 317 19-NOV-2002;
FEATURES            Location/Qualifiers
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ORIGIN

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  Matches   17;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          3 GGGGACUAUACCGCGUAAUGCUGCCUCCCC 32
              || ||  :  || ||  : |:||: ||:|||| 
Db        104 GGAGATTGGACGGCCTGATGCTCCCTCCCC 133


RESULT 8
AR281229
LOCUS       AR281229                196 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 317 from patent US 6518256.
ACCESSION   AR281229
VERSION     AR281229.1  GI:29716706
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 196)
  AUTHORS   Wang,T., Fan,L., Kalos,M.D., Bangur,C.S., Hosken,N.A. and
            Fanger,G.R.
  TITLE     Compounds and methods for therapy and diagnosis of lung cancer
  JOURNAL   Patent: US 6518256-A 317 11-FEB-2003;
FEATURES            Location/Qualifiers
     source         1. .196
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ORIGIN

  Query Match             50.6%;  Score 17.2;  DB 6;  Length 196;
  Best Local Similarity   56.7%;  Pred. No. 8.2e+04;
  Matches   17;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          3 GGGGACUAUACCGCGUAAUGCUGCCUCCCC 32
              || ||  :  || ||  : |:||: ||:|||| 
Db        104 GGAGATTGGACGGCCTGATGCTCCCTCCCC 133


RESULT 9
AX365924
LOCUS       AX365924                196 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 317 from Patent WO0200174.
ACCESSION   AX365924
VERSION     AX365924.1  GI:18697433
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Wang,T., Wang,A., Skeiky,Y.A., Li,S.X., Kalos,M.D., Henderson,R.A.,
            Mcneill,P.D., Fanger,N., Retter,M.W., Marnerakis,M., Fanger,G.R.,
            Vedvick,T.S., Carter,D., Watanabe,Y. and Peckham,D.W.
  TITLE     Compositions and methods for the therapy and diagnosis of lung
            cancer
  JOURNAL   Patent: WO 0200174-A 317 03-JAN-2002;
            CORIXA CORPORATION (US)
FEATURES            Location/Qualifiers
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ORIGIN

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  Matches   17;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          3 GGGGACUAUACCGCGUAAUGCUGCCUCCCC 32
              || ||  :  || ||  : |:||: ||:|||| 
Db        104 GGAGATTGGACGGCCTGATGCTCCCTCCCC 133


RESULT 10
S42430
LOCUS       S42430                   104 bp    DNA     linear   ROD 08-MAY-1993
DEFINITION  T cell receptor alpha chain, T cell receptor alpha chain
            {nonproductive rearrangement} [mice, HLA-Cw3-reactive CTL clone
            Cw3/1.1, Genomic, 104 nt].
ACCESSION   S42430
VERSION     S42430.1  GI:253590
KEYWORDS    .
SOURCE      Mus sp.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 104)
  AUTHORS   Casanova,J.L., Cerottini,J.C., Matthes,M., Necker,A., Gournier,H.,
            Barra,C., Widmann,C., MacDonald,H.R., Lemonnier,F., Malissen,B.
            et,al.
  TITLE     H-2-restricted cytolytic T lymphocytes specific for HLA display T
            cell receptors of limited diversity
  JOURNAL   J. Exp. Med. 176 (2), 439-447 (1992)
  MEDLINE   92364546
   PUBMED   1380061
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 111091] from the original journal article.
            This sequence comes from Fig. 3B.
FEATURES             Location/Qualifiers
     source          1. .104
                     /organism="Mus sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10095"
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                     /note="This sequence comes from Fig. 3B"
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                     /db_xref="GI:253591"
                     /translation="HPGDSAAYFCAVKILEEAMQS"
     gene            39. .101
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     CDS             39. .101
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ORIGIN

  Query Match             50.0%;  Score 17;  DB 10;  Length 104;
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  Matches   15;  Conservative    5;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 UGGGGACUAUACCGCGUAAUGCUGC 26
              :||||||:   |||||:| : |:||
Db          6 TGGGGACTCAGCCGCGTACTTCTGC 30


RESULT 11
MMU26786
LOCUS       MMU26786                 123 bp    mRNA    linear   ROD 18-JUL-2001
DEFINITION  Mus musculus T cell receptor Va5/Ja36 alpha chain mRNA, isolate
            727-6, partial cds.
ACCESSION   U26786
VERSION     U26786.1  GI:847922
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 123)
  AUTHORS   Shih,F.F., Cerasoli,D.M. and Caton,A.J.
  TITLE     A major T cell determinant from the influenza virus hemagglutinin
            (HA) can be a cryptic self peptide in HA transgenic mice
  JOURNAL   Int. Immunol. 9 (2), 249-261 (1997)
  MEDLINE   97192188
   PUBMED   9040007
REFERENCE   2  (bases 1 to 123)
  AUTHORS   Shih,F.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-MAY-1995) Fei F. Shih, The Wistar Institute of
            Anatomy and Chemistry, 3601 Spruce Street, Philadelphia, PA 19104,
            USA
FEATURES             Location/Qualifiers
     source          1. .123
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                     /cell_type="T-helper cell, hybridoma"
     CDS             <1. .>123
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                     /product="T cell receptor Va5/Ja36 alpha chain"
                     /protein_id="AAA67979.1"
                     /db_xref="GI:847923"
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ORIGIN

  Query Match             50.0%;  Score 17;  DB 10;  Length 123;
  Best Local Similarity   60.0%;  Pred. No. 1.2e+05;
  Matches   15;  Conservative    5;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 UGGGGACUAUACCGCGUAAUGCUGC 26
              :||||||:   |||||:| : |:||
Db         33 TGGGGACTCAGCCGCGTACTTCTGC 57


RESULT 12
AY089788
LOCUS       AY089788                 135 bp    mRNA    linear   ROD 01-OCT-2002
DEFINITION  Mus musculus TRP-2 specific T-cell receptor AV5 mRNA, partial cds.
ACCESSION   AY089788
VERSION     AY089788.1  GI:23428649
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 135)
  AUTHORS   De Palma,R., Del Galdo,F., Milan,G. and Bronte,V.
  TITLE     Analysis of T cell receptor repertoire of CTL recognizing the mouse
            melanocyte differentiation antigen TRP-2
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 135)
  AUTHORS   De Palma,R., Del Galdo,F., Milan,G. and Bronte,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-MAR-2002) Clinical and Experimental Medicine, II
            University of Naples, S. Pansini 5, Naples 80131, Italy
FEATURES             Location/Qualifiers
     source          1. .135
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ORIGIN

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  Matches   15;  Conservative    5;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 UGGGGACUAUACCGCGUAAUGCUGC 26
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Db          9 TGGGGACTCAGCCGCGTACTTCTGC 33


RESULT 13
AF012183
LOCUS       AF012183                 157 bp    mRNA    linear   ROD 26-NOV-2001
DEFINITION  Mus musculus T-cell receptor alpha chain (TCRA) mRNA, partial cds.
ACCESSION   AF012183
VERSION     AF012183.1  GI:2331194
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 157)
  AUTHORS   Lin,W.L., Kuzmak,J., Pappas,J., Peng,G., Chernajovsky,Y.,
            Platsoucas,C.D. and Oleszak,E.L.
  TITLE     Amplification of T-cell receptor alpha- and beta-chain transcripts
            from mouse spleen lymphocytes by the nonpalindromic
            adaptor-polymerase chain reaction
  JOURNAL   Unpublished
  MEDLINE   98271283
   PUBMED   9608356
REFERENCE   2  (bases 1 to 157)
  AUTHORS   Lin,W.L., Kuzmak,J., Pappas,J., Chernajovsky,Y., Platsoucas,C.D.
            and Oleszak,E.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUL-1997) Fels Institute for Cancer Research and
            Molecular Biology, Temple University School of Medicine, 3420 North
            Broad Street, Philadelphia, PA 19140, USA
FEATURES             Location/Qualifiers
     source          1. .157
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                     /mol_type="mRNA"
                     /strain="SJL"
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                     /protein_id="AAB66867.1"
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                     /note="V_region 5.3"
     J_segment       103. .152
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ORIGIN

  Query Match             50.0%;  Score 17;  DB 10;  Length 157;
  Best Local Similarity   60.0%;  Pred. No. 1.1e+05;
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Qy          2 UGGGGACUAUACCGCGUAAUGCUGC 26
              :||||||:   |||||:| : |:||
Db         66 TGGGGACTCAGCCGCGTACTTCTGC 90


RESULT 14
AU048750
LOCUS       AU048750                 176 bp    DNA     linear   STS 20-JAN-2000
DEFINITION  Rattus norvegicus, OTSUKA clone, 765a11, microsatellite sequence,
            sequence tagged site.
ACCESSION   AU048750
VERSION     AU048750.1  GI:6721921
KEYWORDS    STS.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (sites)
  AUTHORS   Watanabe,T.K., Hishigaki,H., Okuno,S., Mizoguchi,A., Oga,K.,
            Tsuji,A., Ono,T., Yamasaki,Y., Kanemoto,N., Takahashi,E., Irie,Y.,
            Nakamura,Y., Takagi,Y. and Tanigami,A.
  TITLE     The large-scale mapping of rat microsatellite markers
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 176)
  AUTHORS   Watanabe,T.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-DEC-1998) Takeshi K Watanabe, Otsuka GEN Research
            Institute, Otsuka Pharmaceutical Co., Ltd; 463-10, Kagasuno,
            Kawauchi-cho, Tokushima, Tokushima 771-0192, Japan
            (E-mail:watanabe@otsuka.gr.jp, Tel:+81-886-65-2888,
            Fax:+81-886-37-1035)
FEATURES             Location/Qualifiers
     source          1. .176
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ORIGIN

  Query Match             50.0%;  Score 17;  DB 11;  Length 176;
  Best Local Similarity   60.0%;  Pred. No. 1e+05;
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Qy          5 GGACUAUACCGCGUAAUGCUGCCUC 29
              || |:|:|| | | ||:| :|||:|
Db         36 GGGCTATACAGAGAAATGTTGCCTC 60


RESULT 15
PCH543747
LOCUS       PCH543747                186 bp    mRNA    linear   PLN 12-FEB-2003
DEFINITION  Phanerochaete chrysosporium partial mRNA for putative Hsp70 protein
            (hsp70 gene).
ACCESSION   AJ543747
VERSION     AJ543747.1  GI:28372047
KEYWORDS    hsp70 gene; Hsp70 protein.
SOURCE      Phanerochaete chrysosporium (anamorph: Sporotrichum pruinosum)
  ORGANISM  Phanerochaete chrysosporium
            Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
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            Aphyllophorales; Corticiaceae; Phanerochaete.
REFERENCE   1
  AUTHORS   Assmann,E.M.
  TITLE     Iron-responsive genes in Phanerochaete chrysosporium
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 186)
  AUTHORS   Assmann,E.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-FEB-2003) Assmann E.M., Cbmeg, Universidade Estadual
            de Campinas, Caixa Postal 6010, Campinas, Sao Paulo, 13093-020,
            BRAZIL
FEATURES             Location/Qualifiers
     source          1. .186
                     /organism="Phanerochaete chrysosporium"
                     /mol_type="mRNA"
                     /db_xref="taxon:5306"
     gene            1. .186
                     /gene="hsp70"
     CDS             <1. .>186
                     /gene="hsp70"
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                     /product="putative Hsp70 protein"
                     /protein_id="CAD66422.1"
                     /db_xref="GI:28372048"
                     /translation="ALLIVPPSHRQXCCHRMGQGVLIIDAGGGTVDLSSYCFISLSPI
                     AVEETAPXNERGAYLLEL"
ORIGIN

  Query Match             50.0%;  Score 17;  DB 8;  Length 186;
  Best Local Similarity   48.5%;  Pred. No. 1e+05;
  Matches   16;  Conservative    7;  Mismatches   10;  Indels    0;  Gaps    0;

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              :| ||||:  | | ||:| :||: | :| || :
Db         90 TGTGGACTTGAGCTCGTACTGCTTCATCTCCTT 122


Search completed: April  9, 2004, 03:53:27
Job time : 286.067 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 9, 2004, 01:39:24 ; Search time 120.8 Seconds
(without alignments)
1195.685 Million cell updates/sec

Title: US-09-963-827B-70
Perfect score: 34
Sequence: 1 auggggacuauaccgcguaaugcugccuccccau 34

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 3774412

Minimum DB seq length: 0
Maximum DB seq length: 200

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
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2: geneseqn1990s:*
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4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	34	100.0	34	6	ABN88557	Abn88557 Coagulati
	2	34	100.0	35	7	ABZ21241	Abz21241 FIXa apta
	3	34	100.0	38	7	ABZ21259	Abz21259 Tailed ap
	4	34	100.0	40	7	ABZ21242	Abz21242 FIXa apta
	5	34	100.0	96	6	ABN88490	Abn88490 Coagulati
c	6	21	61.8	23	7	ABZ21269	Abz21269 FIXa apta
	7	17.2	50.6	77	3	AAC14048	Aac14048 Human sec
c	8	17.2	50.6	100	7	ACD79614	Acd79614 E. coli K
	9	17.2	50.6	196	3	AAC66013	Aac66013 Human lun
	10	17.2	50.6	196	6	ABL49232	Abl49232 Human lun
	11	17.2	50.6	196	6	ABQ92418	Abq92418 Human lun
	12	17.2	50.6	196	8	ADA28407	Ada28407 Human lun
c	13	17	50.0	17	7	ABZ21265	Abz21265 FIXa apta
c	14	17	50.0	17	7	ABZ21277	Abz21277 FIXa apta
c	15	17	50.0	18	7	ABZ21266	Abz21266 FIXa apta
c	16	17	50.0	20	7	ABZ21260	Abz21260 Antidote
	17	17	50.0	46	2	AAT43544	Aat43544 Primer 29
c	18	17	50.0	112	4	AAI24741	Aai24741 Probe #14
c	19	17	50.0	112	4	ABA70029	Aba70029 Human foe
c	20	17	50.0	112	4	AAI50142	Aai50142 Probe #18
c	21	17	50.0	112	4	ABA36840	Aba36840 Probe #15
c	22	17	50.0	112	4	AAK44134	Aak44134 Human bon
c	23	17	50.0	112	4	AAK18238	Aak18238 Human bra
c	24	17	50.0	112	4	ABS43790	Abs43790 Human liv
c	25	17	50.0	112	6	ABS18369	Abs18369 Human gen
c	26	16.2	47.6	113	4	ABA69564	Aba69564 Human foe
c	27	16.2	47.6	113	4	AAK43625	Aak43625 Human bon
c	28	16.2	47.6	113	4	AAK17785	Aak17785 Human bra
c	29	16.2	47.6	148	4	AAK67210	Aak67210 Human imm
	30	15.8	46.5	51	4	AAL31035	Aal31035 Human SNP
	31	15.6	45.9	31	7	ABZ21244	Abz21244 FIXa apta
	32	15.6	45.9	33	7	ABZ21258	Abz21258 Aptamer 9
	33	15.6	45.9	76	4	AAS48228	Aas48228 Enterococ
	34	15.6	45.9	76	7	ACA12905	Aca12905 Prokaryot
c	35	15.6	45.9	141	3	AAC24799	Aac24799 Human sec
c	36	15.6	45.9	144	6	ABQ90618	Abq90618 M. capsul
	37	15.6	45.9	164	4	AAI21015	Aai21015 Probe #10
	38	15.6	45.9	164	4	ABA66087	Aba66087 Human foe
	39	15.6	45.9	164	4	AAI46268	Aai46268 Probe #14
	40	15.6	45.9	164	4	ABA48207	Aba48207 Human bre
	41	15.6	45.9	164	4	ABA33163	Aba33163 Probe #11
	42	15.6	45.9	164	4	AAK40252	Aak40252 Human bon
	43	15.6	45.9	164	4	AAK14510	Aak14510 Human bra
	44	15.6	45.9	164	4	ABS39826	Abs39826 Human liv
	45	15.6	45.9	164	5	AAI06732	Aai06732 Probe #67

ALIGNMENTS

RESULT 1
ABN88557
ID ABN88557 standard; RNA; 34 BP.
XX
AC ABN88557;
XX
DT 19-AUG-2002 (first entry)
XX
DE Coagulation factor IXa (FIXa) aptamer SEQ ID NO:70.
XX
KW RNA aptamer; identification; coagulation factor; angiopoietin; thrombin;
KW E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant;
KW cell proliferation; intimal hyperplasia; angiogenesis;
KW bypass graft surgery; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200226932-A2.
XX
PD 04-APR-2002.
XX
PF 26-SEP-2001; 2001WO-US030004.
XX
PR 26-SEP-2000; 2000US-0235654P.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Sullenger BA, Rusconi CP;
XX
DR WPI; 2002-479560/51.
XX
PT Novel RNA aptamers that selectively bind coagulation pathway factors, E2F
PT family members, Ang1 or Ang2, useful for modulating coagulation pathway
PT factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.
XX
PS Claim 14; Page 25; 216pp; English.
XX
CC The present invention describes RNA aptamers (I,II,III) that selectively
CC bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c)
CC angiopoietin-1 (Ang1) or Ang2, respectively, where (I), (II), (III) have
CC a dissociation constant for the coagulation pathway factor, an E2F family
CC member, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) have
CC cardiant and cytostatic activities. (I) are useful for modulating the
CC biological activity of a coagulation pathway factor which involves
CC administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that

```
CC   the biological activity of the coagulation pathway factor in the warm-
CC   blooded vertebrate is modulated. (I) are also useful for treating
CC   cardiovascular diseases in the mammal. (II) are useful for modulating E2F
CC   activity in a warm-blooded vertebrate. (III) are useful for modulating
CC   Ang1 or Ang2 activity in a warm-blooded vertebrate. (I) are potent
CC   anticoagulants and significantly delay the clotting time of normal human
CC   plasma or the activation of platelets in response to thrombin. (II) are
CC   useful for inhibiting cell proliferation in a number of conditions e.g.,
CC   intimal hyperplasia following bypass graft surgery. (III) are useful for
CC   modulating angiogenesis. The RNA aptamers are also useful for diagnostic,
CC   research and therapeutic context. The aptamers are useful as diagnostic
CC   reagents to detect the presence or absence of target substances to which
CC   they specifically bind, and for identifying substances to which they
CC   specifically bind, for isolating and purifying substances to which they
CC   bind, and as a separation reagent for retrieving the targets to which
CC   they specifically bind. ABN88488 to ABN88713 and ABB81231 represent
CC   sequences used in the exemplification of the present invention
XX
SQ   Sequence 34 BP; 7 A; 11 C; 8 G; 0 T; 8 U; 0 Other;

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  Best Local Similarity   100.0%;  Pred. No. 6.7e-06;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||||||||||||||
Db          1 AUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAU 34


RESULT 2
ABZ21241
ID   ABZ21241 standard; RNA; 35 BP.
XX
AC   ABZ21241;
XX
DT   16-APR-2003  (first entry)
XX
DE   FIXa aptamer, 9.3t, SEQ ID 1.
XX
KW   Immunosuppressive; aptamer; infection; autoimmunity; tumour;
KW   inflammatory proliferative disease; hypoglycaemia; human;
KW   coagulation Factor IXa; FIXa; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
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FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "All purines are 2'hydroxyl and pyrimidines are 2'
FT                    -fluoro nucleotides"
FT   misc_binding     1. .7
FT                    /*tag=  b
FT                    /bound_moiety= "Nucleotides 28. .34"
FT   stem_loop        15. .26
FT                    /*tag=  c
FT   misc_binding     28. .34
FT                    /*tag=  d
FT                    /bound_moiety= "Nucleotides 1. .7"
FT   modified_base    35
FT                    /*tag=  e
FT                    /mod_base= OTHER
FT                    /note= "idT"
XX
PN   WO200296926-A1.
XX
PD   05-DEC-2002.
XX
PF   28-MAY-2002; 2002WO-US016555.
XX
PR   25-MAY-2001; 2001US-0293231P.
PR   07-NOV-2001; 2001US-0331037P.
XX
PA   (UYDU-) UNIV DUKE.
XX
PI   Sullenger BA,  Rusconi C;
XX
DR   WPI; 2003-140438/13.
XX
PT   Altering affinity of nucleic acid ligands for target molecules in a
PT   patient or reversing binding of labeled ligands to target tissues, by
PT   administering (to a patient receiving the ligand) a modulator that binds
PT   to ligand.
XX
PS   Example 1; Fig 1; 111pp; English.
XX
CC   The present invention relates to a method for altering the affinity of a
CC   nucleic acid ligand (e.g. an aptamer) for a target molecule in a patient
CC   or in vitro, or reversing the binding of the labelled ligand to a target
CC   tissue. The method comprises administering a modulator that binds to the
CC   ligand to a patient receiving the ligand, or contacting the ligand with
CC   the modulator under conditions such that the modulator binds to the
CC   ligand, and thus alters the affinity of the ligand for the target
CC   molecule. The method is useful for treating a number of disorders e.g.
CC   infection, autoimmunity, tumours, inflammatory proliferative diseases and
CC   hypoglycaemia. The present sequence is a nuclease-resistant 2'-fluoro
CC   pyrimidine-modified aptamer to human coagulation Factor IXa (FIXa
CC   aptamer), which was used to illustrate the method of the invention
XX
SQ   Sequence 35 BP; 7 A; 11 C; 8 G; 1 T; 8 U; 0 Other;

  Query Match             100.0%;  Score 34;  DB 7;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 6.8e-06;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||||||||||||||
Db          1 AUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAU 34


RESULT 3
ABZ21259
ID   ABZ21259 standard; RNA; 38 BP.
XX
AC   ABZ21259;
XX
DT   16-APR-2003  (first entry)
XX
DE   Tailed aptamer 9.3t-3NT, SEQ ID 19.
XX
KW   Immunosuppressive; aptamer; infection; autoimmunity; tumour;
KW   inflammatory proliferative disease; hypoglycaemia; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_binding     1. .7
FT                    /*tag=  a
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FT   stem_loop        15. .26
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FT                    /note= "mG mU mC idT"
XX
PN   WO200296926-A1.
XX
PD   05-DEC-2002.
XX
PF   28-MAY-2002; 2002WO-US016555.
XX
PR   25-MAY-2001; 2001US-0293231P.
```

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PR   07-NOV-2001; 2001US-0331037P.
XX
PA   (UYDU-) UNIV DUKE.
XX
PI   Sullenger BA,  Rusconi C;
XX
DR   WPI; 2003-140438/13.
XX
PT   Altering affinity of nucleic acid ligands for target molecules in a
PT   patient or reversing binding of labeled ligands to target tissues, by
PT   administering (to a patient receiving the ligand) a modulator that binds
PT   to ligand.
XX
PS   Example 4; Fig 11; 111pp; English.
XX
CC   The present invention relates to a method for altering the affinity of a
CC   nucleic acid ligand (e.g. an aptamer) for a target molecule in a patient
CC   or in vitro, or reversing the binding of the labelled ligand to a target
CC   tissue. The method comprises administering a modulator that binds to the
CC   ligand to a patient receiving the ligand, or contacting the ligand with
CC   the modulator under conditions such that the modulator binds to the
CC   ligand, and thus alters the affinity of the ligand for the target
CC   molecule. The method is useful for treating a number of disorders e.g.
CC   infection, autoimmunity, tumours, inflammatory proliferative diseases and
CC   hypoglycaemia. The present sequence is an aptamer which was used to
CC   illustrate the method of the invention
XX
SQ   Sequence 38 BP; 7 A; 12 C; 9 G; 1 T; 9 U; 0 Other;

  Query Match             100.0%;  Score 34;  DB 7;  Length 38;
  Best Local Similarity   100.0%;  Pred. No. 6.9e-06;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAU 34
              ||||||||||||||||||||||||||||||||||
Db          1 AUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAU 34


RESULT 4
ABZ21242
ID   ABZ21242 standard; RNA; 40 BP.
XX
AC   ABZ21242;
XX
DT   16-APR-2003  (first entry)
XX
DE   FIXa aptamer, SEQ ID 2.
XX
KW   Immunosuppressive; aptamer; infection; autoimmunity; tumour;
KW   inflammatory proliferative disease; hypoglycaemia; human;
KW   coagulation Factor IXa; FIXa; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_binding     1. .10
FT                    /*tag=  a
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FT   stem_loop        18. .29
FT                    /*tag=  b
FT   misc_binding     31. .40
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XX
PN   WO200296926-A1.
XX
PD   05-DEC-2002.
XX
PF   28-MAY-2002; 2002WO-US016555.
XX
PR   25-MAY-2001; 2001US-0293231P.
PR   07-NOV-2001; 2001US-0331037P.
XX
PA   (UYDU-) UNIV DUKE.
XX
PI   Sullenger BA,  Rusconi C;
XX
DR   WPI; 2003-140438/13.
XX
PT   Altering affinity of nucleic acid ligands for target molecules in a
PT   patient or reversing binding of labeled ligands to target tissues, by
PT   administering (to a patient receiving the ligand) a modulator that binds
PT   to ligand.
XX
PS   Example 2; Fig 7; 111pp; English.
XX
CC   The present invention relates to a method for altering the affinity of a
CC   nucleic acid ligand (e.g. an aptamer) for a target molecule in a patient
CC   or in vitro, or reversing the binding of the labelled ligand to a target
CC   tissue. The method comprises administering a modulator that binds to the
CC   ligand to a patient receiving the ligand, or contacting the ligand with
CC   the modulator under conditions such that the modulator binds to the
CC   ligand, and thus alters the affinity of the ligand for the target
CC   molecule. The method is useful for treating a number of disorders e.g.
CC   infection, autoimmunity, tumours, inflammatory proliferative diseases and
CC   hypoglycaemia. The present sequence is an aptamer to human coagulation
CC   Factor IXa (FIXa aptamer), which was used to illustrate the method of the
CC   invention
XX
SQ   Sequence 40 BP; 7 A; 13 C; 11 G; 0 T; 9 U; 0 Other;

  Query Match             100.0%;  Score 34;  DB 7;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 6.9e-06;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAU 34
              ||||||||||||||||||||||||||||||||||
Db          4 AUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAU 37


RESULT 5
ABN88490
ID   ABN88490 standard; RNA; 96 BP.
XX
AC   ABN88490;
XX
DT   19-AUG-2002  (first entry)
XX
DE   Coagulation factor IXa binding/inhibiting RNA aptamer SEQ ID NO:3.
XX
KW   RNA aptamer; identification; coagulation factor; angiopoietin; thrombin;
KW   E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant;
KW   cell proliferation; intimal hyperplasia; angiogenesis;
KW   bypass graft surgery; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200226932-A2.
XX
PD   04-APR-2002.
XX
PF   26-SEP-2001; 2001WO-US030004.
XX
PR   26-SEP-2000; 2000US-0235654P.
XX
PA   (UYDU-) UNIV DUKE.
XX
PI   Sullenger BA,  Rusconi CP;
XX
DR   WPI; 2002-479560/51.
XX
PT   Novel RNA aptamers that selectively bind coagulation pathway factors, E2F
PT   family members, Ang1 or Ang2, useful for modulating coagulation pathway
PT   factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.
XX
```

```
PS   Claim 13; Fig 1A; 216pp; English.
XX
CC   The present invention describes RNA aptamers (I,II,III) that selectively
CC   bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c)
CC   angiopoietin-1 (Ang1) or Ang2, respectively, where (I), (II), (III) have
CC   a dissociation constant for the coagulation pathway factor, an E2F family
CC   member, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) have
CC   cardiant and cytostatic activities. (I) are useful for modulating the
CC   biological activity of a coagulation pathway factor which involves
CC   administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that
CC   the biological activity of the coagulation pathway factor in the warm-
CC   blooded vertebrate is modulated. (I) are also useful for treating
CC   cardiovascular diseases in the mammal. (II) are useful for modulating E2F
CC   activity in a warm-blooded vertebrate. (III) are useful for modulating
CC   Ang1 or Ang2 activity in a warm-blooded vertebrate. (I) are potent
CC   anticoagulants and significantly delay the clotting time of normal human
CC   plasma or the activation of platelets in response to thrombin. (II) are
CC   useful for inhibiting cell proliferation in a number of conditions e.g.,
CC   intimal hyperplasia following bypass graft surgery. (III) are useful for
CC   modulating angiogenesis. The RNA aptamers are also useful for diagnostic,
CC   research and therapeutic context. The aptamers are useful as diagnostic
CC   reagents to detect the presence or absence of target substances to which
CC   they specifically bind, and for identifying substances to which they
CC   specifically bind, for isolating and purifying substances to which they
CC   bind, and as a separation reagent for retrieving the targets to which
CC   they specifically bind. ABN88488 to ABN88713 and ABB81231 represent
CC   sequences used in the exemplification of the present invention
XX
SQ   Sequence 96 BP; 24 A; 27 C; 29 G; 0 T; 16 U; 0 Other;

  Query Match            100.0%;  Score 34;  DB 6;  Length 96;
  Best Local Similarity  100.0%;  Pred. No. 8.1e-06;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAU 34
              ||||||||||||||||||||||||||||||||||
Db         18 AUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAU 51


RESULT 6
ABZ21269/c
ID   ABZ21269 standard; RNA; 23 BP.
XX
AC   ABZ21269;
XX
DT   16-APR-2003  (first entry)
XX
DE   FIXa aptamer 9.3t&9.3t-3NT oligonucleotide modulator, AS 5-1, SEQ ID 29.
XX
KW   Immunosuppressive; aptamer; infection; autoimmunity; tumour;
KW   inflammatory proliferative disease; hypoglycaemia; human;
KW   coagulation Factor IXa; FIXa; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .23
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "All nucleotides are 2'Omethyl oligonucleotides"
XX
PN   WO200296926-A1.
XX
PD   05-DEC-2002.
XX
PF   28-MAY-2002; 2002WO-US016555.
XX
PR   25-MAY-2001; 2001US-0293231P.
PR   07-NOV-2001; 2001US-0331037P.
XX
PA   (UYDU-) UNIV DUKE.
XX
PI   Sullenger BA,  Rusconi C;
XX
DR   WPI; 2003-140438/13.
XX
PT   Altering affinity of nucleic acid ligands for target molecules in a
PT   patient or reversing binding of labeled ligands to target tissues, by
PT   administering (to a patient receiving the ligand) a modulator that binds
PT   to ligand.
XX
PS   Claim 50; Page 74; 111pp; English.
XX
CC   The present invention relates to a method for altering the affinity of a
CC   nucleic acid ligand (e.g. an aptamer) for a target molecule in a patient
CC   or in vitro, or reversing the binding of the labelled ligand to a target
CC   tissue. The method comprises administering a modulator that binds to the
CC   ligand to a patient receiving the ligand, or contacting the ligand with
CC   the modulator under conditions such that the modulator binds to the
CC   ligand, and thus alters the affinity of the ligand for the target
CC   molecule. The method is useful for treating a number of disorders e.g.
CC   infection, autoimmunity, tumours, inflammatory proliferative diseases and
CC   hypoglycaemia. The present sequence is an oligonucleotide modulator,
CC   which targets the FIXa aptamers 9.3t and 9.3t-3NT. The FIXa aptamers bind
CC   to human coagulation Factor IXa and were used to illustrate the method of
CC   the invention. This oligonucleotide was found to be effective at
CC   reversing FIXa aptamer's anticoagulation activity in human plasma in
CC   vitro
XX
SQ   Sequence 23 BP; 5 A; 7 C; 5 G; 0 T; 6 U; 0 Other;

  Query Match            61.8%;  Score 21;  DB 7;  Length 23;
  Best Local Similarity  81.0%;  Pred. No. 6.4;
  Matches   17;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GGGGACUAUACCGCGUAAUGC 23
              ||||||:|:||||||:||:||
Db         21 GGGGACTATACCGCGTAATGC 1


RESULT 7
AAC14048
ID   AAC14048 standard; cDNA; 77 BP.
XX
AC   AAC14048;
XX
DT   06-OCT-2000  (first entry)
XX
DE   Human secreted protein 5' EST, SEQ ID NO: 18123.
XX
KW   Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW   gene therapy; chromosome mapping; ss.
XX
OS   Homo sapiens.
XX
PN   EP1033401-A2.
XX
PD   06-SEP-2000.
XX
PF   21-FEB-2000; 2000EP-00200610.
XX
PR   26-FEB-1999;   99US-0122487P.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J,  Duclert A,  Giordano J;
XX
DR   WPI; 2000-500381/45.
XX
PT   New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT   obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT   diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
PS   Claim 1; SEQ ID NO 18123; 71pp + Sequence Listing; English.
XX
CC   The present sequence is one of a large number of 5' ESTs derived from
```

```
CC   mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC   identified within the present sequence. The 5' ESTs were prepared from
CC   total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC   sequences usually correspond mainly to the 3' untranslated region (UTR)
CC   of the mRNA because they are often obtained from oligo-dT primed cDNA
CC   libraries. Such ESTs are not well suited for isolating cDNA sequences
CC   derived from the 5' ends of mRNAs and even in those cases where longer
CC   cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
CC   ESTs are derived from mRNAs with intact 5' ends and can therefore be used
CC   to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
CC   diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC   They are used to obtain upstream regulatory sequences and to design
CC   expression and secretion vectors
XX
SQ   Sequence 77 BP; 31 A; 16 C; 14 G; 16 T; 0 U; 0 Other;

  Query Match             50.6%;  Score 17.2;  DB 3;  Length 77;
  Best Local Similarity   56.7%;  Pred. No. 4.5e+02;
  Matches   17;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          2 UGGGGACUAUACCGCGUAAUGCUGCCUCCC 31
              :||| ||:|:  |  | ||  |:|||:|||
Db          4 TGGGAACTATGTCAGGAAAACCTGCCTCCC 33


RESULT 8
ACD79614/c
ID   ACD79614 standard; DNA; 100 BP.
XX
AC   ACD79614;
XX
DT   19-SEP-2003  (first entry)
XX
DE   E. coli K12 MG1655 biochip probe SEQ ID 10890.
XX
KW   Biochip; gene expression; gut; diagnostic; detection; probe; ss.
XX
OS   Escherichia coli.
XX
PN   EP1260592-A1.
XX
PD   27-NOV-2002.
XX
PF   17-MAY-2001; 2001EP-00112179.
XX
PR   17-MAY-2001; 2001EP-00112179.
XX
PA   (MWGB-) MWG-BIOTECH AG.
XX
PI   Donner H,  Drescher B,  Huber A,  Weber J;
XX
DR   WPI; 2003-241155/24.
XX
PT   Biochip containing probes complementary with open reading frames in
PT   Escherichia coli K12, useful for detecting gene expression and expression
PT   patterns.
XX
PS   Claim 3; Page 1697; 2004pp; German.
XX
CC   This invention describes a novel biochip comprising probe spots, each
CC   containing many identical probes. The probes are nucleotide sequences of
CC   30-80 bases, are prepared ex situ from synthetic oligonucleotides and at
CC   least one includes a segment of at least 20 bases identical with, or
CC   complementary to, a segment of an open reading frame (orf) of Escherichia
CC   coli K12. The biochip is used for specific detection of gene expression
CC   in K12 and for determining the gene expression pattern, e.g. for
CC   diagnostic determination of which E. coli strains are present in the gut,
CC   and to determine the effects of e.g. growth media on gene expression. The
CC   biochip provides as comprehensive as possible detection of the K12
CC   genome, with simultaneous analysis of many different genes with a single
CC   device, and comparison of gene expression between K12 and its mutants or
CC   other E. coli strains in a single experiment. Apart from qualitative and
CC   quantitative information about gene expression, it also allows
CC   measurements of population densities for the various strains. The use of
CC   synthetic oligonucleotides for preparation of probes allows free
CC   variation in probe length and ensures high purity (and thus selectivity,
CC   reactivity and reproducibility); also synthetic probes are generally
CC   shorter than probes prepared by polymerase chain reaction. ACD68731 to
CC   ACD81540 represent oligonucleotide probes used with the biochip described
CC   in the invention
XX
SQ   Sequence 100 BP; 23 A; 21 C; 31 G; 25 T; 0 U; 0 Other;

  Query Match             50.6%;  Score 17.2;  DB 7;  Length 100;
  Best Local Similarity   60.0%;  Pred. No. 4.7e+02;
  Matches   18;  Conservative    4;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 AUGGGGACUAUACCGCGUAAUGCUGCCUCC 30
              |:|| ||  | | ||||:||:|| | |: |
Db         82 ATGGCGATGAAATCGCGTAATGCCGGCTTC 53


RESULT 9
AAC66013
ID   AAC66013 standard; cDNA; 196 BP.
XX
AC   AAC66013;
XX
DT   21-FEB-2001  (first entry)
XX
DE   Human lung cancer-associated cDNA clone 25331.
XX
KW   Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
KW   vaccine; detection; ss.
XX
OS   Homo sapiens.
XX
PN   WO200061612-A2.
XX
PD   19-OCT-2000.
XX
PF   03-APR-2000; 2000WO-US008896.
XX
PR   02-APR-1999;   99US-00285479.
PR   17-DEC-1999;   99US-00466396.
PR   30-DEC-1999;   99US-00476496.
PR   10-JAN-2000; 2000US-00480884.
PR   22-FEB-2000; 2000US-00510376.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Wang T,  Fan L;
XX
DR   WPI; 2000-628399/60.
XX
PT   Isolated polypeptide comprising an immunogenic portion of a lung tumor
PT   protein is used for detecting and monitoring progression of lung cancer
PT   in a patient.
XX
PS   Claim 1a; Page 233; 261pp; English.
XX
CC   This invention describes a novel isolated polypeptide (I) which
CC   comprising an immunogenic portion of a lung tumor protein or variant (P2)
CC   which have cytostatic activity. The polypeptides and polynucleotides are
CC   used in compositions and vaccines to inhibit the development of cancer,
CC   especially lung cancer, in a patient. Methods described in the invention
CC   can be used to monitor the progression of a cancer by carrying out the
CC   detection at subsequent time points and comparing the results from the
CC   different time points. CD4+ and/or CD8+ T-Cells isolated from a patient
CC   are treated with P2, polynucleotides encoding P2 or antigen presenting
CC   cells expressing P2 and then administered to the patient to inhibit
CC   development of cancer
XX
SQ   Sequence 196 BP; 29 A; 52 C; 62 G; 53 T; 0 U; 0 Other;

  Query Match             50.6%;  Score 17.2;  DB 3;  Length 196;
```

```
  Best Local Similarity   56.7%;  Pred. No. 5.4e+02;
  Matches   17;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          3 GGGGACUAUACCGCGUAAUGCUGCCUCCCC 32
              || ||  :  || ||  : |:||: ||:|||| 
Db        104 GGAGATTGGACGGCCTGATGCTCCCTCCCC 133


RESULT 10
ABL49232
ID   ABL49232 standard; cDNA; 196 BP.
XX
AC   ABL49232;
XX
DT   01-MAY-2002  (first entry)
XX
DE   Human lung tumour cDNA sequence clone 25331 SEQ ID NO:317.
XX
KW   Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
KW   immune response; ss.
XX
OS   Homo sapiens.
XX
PN   WO200200174-A2.
XX
PD   03-JAN-2002.
XX
PF   28-JUN-2001; 2001WO-US021065.
XX
PR   28-JUN-2000; 2000US-00606421.
PR   02-AUG-2000; 2000US-00630940.
PR   21-AUG-2000; 2000US-00643597.
PR   15-SEP-2000; 2000US-00662786.
PR   09-OCT-2000; 2000US-00685696.
PR   12-DEC-2000; 2000US-00735705.
PR   07-MAY-2001; 2001US-00850716.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Wang T,  Wang A,  Skeiky YAW,  Li SX,  Kalos MD,  Henderson RA;
PI   Mcneill PD,  Fanger N,  Retter MW,  Marnerakis M,  Fanger GR;
PI   Vedvick TS,  Carter D,  Watanabe Y,  Peckham DW;
XX
DR   WPI; 2002-090513/12.
XX
PT   Polynucleotides encoding lung tumor polypeptides, useful for treating
PT   lung cancer or stimulating an immune response.
XX
PS   Example 1; Page 309-310; 374pp; English.
XX
CC   The present invention describes human lung tumour proteins. Human lung
CC   tumour proteins and polynucleotides have cytostatic and immunostimulant
CC   activities, and can be used in vaccine production. Compositions
CC   comprising the lung tumour proteins, polynucleotides, antibodies, fusion
CC   proteins, T cell populations, or antigen presenting cells that express
CC   the lung tumour proteins are useful for treating lung cancer or
CC   stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to
CC   ABB75070 represent sequences used in the exemplification of the present
CC   invention
XX
SQ   Sequence 196 BP; 29 A; 52 C; 62 G; 53 T; 0 U; 0 Other;

  Query Match             50.6%;  Score 17.2;  DB 6;  Length 196;
  Best Local Similarity   56.7%;  Pred. No. 5.4e+02;
  Matches   17;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          3 GGGGACUAUACCGCGUAAUGCUGCCUCCCC 32
              || ||  :  || ||  : |:||: ||:|||| 
Db        104 GGAGATTGGACGGCCTGATGCTCCCTCCCC 133


RESULT 11
ABQ92418
ID   ABQ92418 standard; cDNA; 196 BP.
XX
AC   ABQ92418;
XX
DT   07-OCT-2002  (first entry)
XX
DE   Human lung cancer associated cDNA sequence SEQ ID NO:317.
XX
KW   Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine; gene;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   WO200247534-A2.
XX
PD   20-JUN-2002.
XX
PF   30-NOV-2001; 2001WO-US047576.
XX
PR   12-DEC-2000; 2000US-00735705.
PR   07-MAY-2001; 2001US-00850716.
PR   28-JUN-2001; 2001US-00897778.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Wang T,  Wang A,  Skeiky YAW,  Li SX,  Kalos MD,  Henderson RA;
PI   Mcneill PD,  Fanger N,  Retter MW,  Durham M,  Fanger GR,  Vedvick TS;
PI   Carter D,  Watanabe Y,  Peckham DW,  Cai F,  Foy TM;
XX
DR   WPI; 2002-583465/62.
XX
PT   Novel lung carcinoma polynucleotide sequences and polypeptides encoded by
PT   the polynucleotides, useful in pharmaceutical compositions such as
PT   vaccines and as markers to indicate the presence of lung cancer.
XX
PS   Example 1; Page 317; 381pp; English.
XX
CC   The present invention describes isolated human lung carcinoma
CC   polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic
CC   activity, and can be used in gene therapy and in vaccines. Compositions
CC   comprising (I) or (II) can be used for stimulating an immune response in
CC   a patient and for treating lung cancer in a patient. Oligonucleotides of
CC   (I) can be used for detecting the presence of a cancer in a patient, by
CC   obtaining a biological sample from the patient, contacting the biological
CC   sample with the oligonucleotide, detecting in the sample, an amount of
CC   polynucleotide that hybridises to the oligonucleotide and comparing the
CC   amount of polynucleotide that hybridises to the oligonucleotide to a
CC   predetermined cut-off value, and determining the presence of a cancer in
CC   the patient. (I) and (II) are useful in pharmaceutical compositions, e.g.
CC   vaccines. (I) is useful as a marker to indicate the presence or absence
CC   of a cancer such as lung cancer. ABQ92145 to ABQ92486 and ABP61866 to
CC   ABP61992 represent sequences used in the exemplification of the present
CC   invention
XX
SQ   Sequence 196 BP; 29 A; 52 C; 62 G; 53 T; 0 U; 0 Other;

  Query Match             50.6%;  Score 17.2;  DB 6;  Length 196;
  Best Local Similarity   56.7%;  Pred. No. 5.4e+02;
  Matches   17;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          3 GGGGACUAUACCGCGUAAUGCUGCCUCCCC 32
              || ||  :  || ||  : |:||: ||:|||| 
Db        104 GGAGATTGGACGGCCTGATGCTCCCTCCCC 133


RESULT 12
ADA28407
ID   ADA28407 standard; cDNA; 196 BP.
XX
AC   ADA28407;
XX
DT   20-NOV-2003  (first entry)
XX
```

```
DE   Human lung tumour DNA clone 25331.
XX
KW   cancer; lung cancer; gene therapy; vaccine; human;
KW   lung squamous cell carcinoma; ss.
XX
OS   Homo sapiens.
XX
PN   US2003064947-A1.
XX
PD   03-APR-2003.
XX
PF   30-NOV-2001; 2001US-00007700.
XX
PR   18-MAR-1998;   98US-00040802.
PR   27-JUL-1998;   98US-00123912.
PR   22-DEC-1998;   98US-00221107.
PR   02-APR-1999;   99US-00285479.
PR   17-DEC-1999;   99US-00466396.
PR   30-DEC-1999;   99US-00476496.
PR   10-JAN-2000; 2000US-00480884.
PR   22-FEB-2000; 2000US-00510376.
PR   04-APR-2000; 2000US-00542615.
PR   28-JUN-2000; 2000US-00606421.
PR   02-AUG-2000; 2000US-00630940.
PR   21-AUG-2000; 2000US-00643597.
PR   15-SEP-2000; 2000US-00662786.
PR   09-OCT-2000; 2000US-00685696.
PR   12-DEC-2000; 2000US-00735705.
PR   07-MAY-2001; 2001US-00850716.
PR   28-JUN-2001; 2001US-00897778.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Wang T,  Wang A,  Skeiky YAW,  Li SX,  Kalos MD,  Henderson RA;
PI   Mcneill PD,  Fanger N,  Retter MW,  Durham M,  Fanger GR,  Vedvick TS;
PI   Carter D,  Watanabe Y,  Peckham DW,  Cai F,  Foy TM;
XX
DR   WPI; 2003-540798/51.
XX
PT   New isolated polynucleotides and polypeptides useful for diagnosing,
PT   preventing and/or treating cancer, particularly lung cancer.
XX
PS   Example 1; Page 224; 296pp; English.
XX
CC   The invention describes isolated polynucleotides and polypeptides useful
CC   for diagnosing, preventing and/or treating cancer, particularly lung
CC   cancer. A new isolated polynucleotide comprises: any of the 22 fully
CC   defined nucleotide sequences (e.g. 1012, 900 or 2773 bp) given in the
CC   specification; complements of the nucleotide sequences cited above; at
CC   least 10 contiguous residues of the nucleotide sequences cited above; a
CC   sequence that hybridise to any of the nucleotide sequences under highly
CC   stringent conditions; a sequence that is at least 75 or 90% identical to
CC   the above nucleotide sequences; or degenerate variants of the above
CC   nucleotide sequences. The composition and methods are useful in
CC   diagnosing, preventing and/or treating cancer, particularly lung cancer,
CC   in gene therapy and in vaccines. This sequence represents a human lung
CC   tumour cDNA isolated from a lung squamous cell carcinoma that may be
CC   useful in the diagnosis and treatment of lung cancer and other disorders.
XX
SQ   Sequence 196 BP; 29 A; 52 C; 62 G; 53 T; 0 U; 0 Other;

  Query Match             50.6%;  Score 17.2;  DB 8;  Length 196;
  Best Local Similarity   56.7%;  Pred. No. 5.4e+02;
  Matches   17;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          3 GGGGACUAUACCGCGUAAUGCUGCCUCCCC 32
              || ||  :  || ||  : |:||: ||:||||
Db        104 GGAGATTGGACGGCCTGATGCTCCCTCCCC 133


RESULT 13
ABZ21265/c
ID   ABZ21265 standard; RNA; 17 BP.
XX
AC   ABZ21265;
XX
DT   16-APR-2003  (first entry)
XX
DE   FIXa aptamer 9.3t oligonucleotide modulator, SEQ ID 25.
XX
KW   Immunosuppressive; aptamer; infection; autoimmunity; tumour;
KW   inflammatory proliferative disease; hypoglycaemia; human;
KW   coagulation Factor IXa; FIXa; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .17
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "All nucleotides are 2'Omethyl oligonucleotides"
XX
PN   WO200296926-A1.
XX
PD   05-DEC-2002.
XX
PF   28-MAY-2002; 2002WO-US016555.
XX
PR   25-MAY-2001; 2001US-0293231P.
PR   07-NOV-2001; 2001US-0331037P.
XX
PA   (UYDU-) UNIV DUKE.
XX
PI   Sullenger BA,  Rusconi C;
XX
DR   WPI; 2003-140438/13.
XX
PT   Altering affinity of nucleic acid ligands for target molecules in a
PT   patient or reversing binding of labeled ligands to target tissues, by
PT   administering (to a patient receiving the ligand) a modulator that binds
PT   to ligand.
XX
PS   Claim 50; Page 71; 111pp; English.
XX
CC   The present invention relates to a method for altering the affinity of a
CC   nucleic acid ligand (e.g. an aptamer) for a target molecule in a patient
CC   or in vitro, or reversing the binding of the labelled ligand to a target
CC   tissue. The method comprises administering a modulator that binds to the
CC   ligand to a patient receiving the ligand, or contacting the ligand with
CC   the modulator under conditions such that the modulator binds to the
CC   ligand, and thus alters the affinity of the ligand for the target
CC   molecule. The method is useful for treating a number of disorders e.g.
CC   infection, autoimmunity, tumours, inflammatory proliferative diseases and
CC   hypoglycaemia. The present sequence is an oligonucleotide modulator,
CC   which targets FIXa aptamer 9.3t. FIXa aptamer binds to human coagulation
CC   Factor IXa and was used to illustrate the method of the invention
XX
SQ   Sequence 17 BP; 5 A; 2 C; 7 G; 0 T; 3 U; 0 Other;

  Query Match             50.0%;  Score 17;  DB 7;  Length 17;
  Best Local Similarity   70.6%;  Pred. No. 4.3e+02;
  Matches   12;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          18 UAAUGCUGCCUCCCCAU 34
               :||:||:|||:|||||:
Db          17 TAATGCTGCCTCCCCAT 1


RESULT 14
ABZ21277/c
ID   ABZ21277 standard; RNA; 17 BP.
XX
AC   ABZ21277;
XX
DT   16-APR-2003  (first entry)
XX
```

```
DE   FIXa aptamer oligonucleotide modulator, 5-2C, SEQ ID 41.
XX
KW   Immunosuppressive; aptamer; infection; autoimmunity; tumour;
KW   inflammatory proliferative disease; hypoglycaemia; human;
KW   coagulation Factor IXa; FIXa; ss.
XX
OS   Unidentified.
XX
PN   WO200296926-A1.
XX
PD   05-DEC-2002.
XX
PF   28-MAY-2002; 2002WO-US016555.
XX
PR   25-MAY-2001; 2001US-0293231P.
PR   07-NOV-2001; 2001US-0331037P.
XX
PA   (UYDU-) UNIV DUKE.
XX
PI   Sullenger BA,  Rusconi C;
XX
DR   WPI; 2003-140438/13.
XX
PT   Altering affinity of nucleic acid ligands for target molecules in a
PT   patient or reversing binding of labeled ligands to target tissues, by
PT   administering (to a patient receiving the ligand) a modulator that binds
PT   to ligand.
XX
PS   Claim 50; Page 75; 111pp; English.
XX
CC   The present invention relates to a method for altering the affinity of a
CC   nucleic acid ligand (e.g. an aptamer) for a target molecule in a patient
CC   or in vitro, or reversing the binding of the labelled ligand to a target
CC   tissue. The method comprises administering a modulator that binds to the
CC   ligand to a patient receiving the ligand, or contacting the ligand with
CC   the modulator under conditions such that the modulator binds to the
CC   ligand, and thus alters the affinity of the ligand for the target
CC   molecule. The method is useful for treating a number of disorders e.g.
CC   infection, autoimmunity, tumours, inflammatory proliferative diseases and
CC   hypoglycaemia. The present sequence is an oligonucleotide modulator,
CC   which targets the FIXa aptamers 9.3t and 9.3t-3NT. The FIXa aptamers bind
CC   to human coagulation Factor IXa and were used to illustrate the method of
CC   the invention. This oligonucleotide was found to be effective at
CC   reversing FIXa aptamer's anticoagulation activity in human plasma in
CC   vitro
XX
SQ   Sequence 17 BP; 3 A; 6 C; 4 G; 0 T; 4 U; 0 Other;

  Query Match             50.0%;  Score 17;  DB 7;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 4.3e+02;
  Matches   14;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

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              |:||||||:|:||||||
Db         17 ATGGGGACTATACCGCG 1


RESULT 15
ABZ21266/c
ID   ABZ21266 standard; RNA; 18 BP.
XX
AC   ABZ21266;
XX
DT   16-APR-2003  (first entry)
XX
DE   FIXa aptamer 9.3t oligonucleotide modulator, Anti D T1, SEQ ID 26.
XX
KW   Immunosuppressive; aptamer; infection; autoimmunity; tumour;
KW   inflammatory proliferative disease; hypoglycaemia; human;
KW   coagulation Factor IXa; FIXa; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
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FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "All nucleotides are 2'Omethyl oligonucleotides"
XX
PN   WO200296926-A1.
XX
PD   05-DEC-2002.
XX
PF   28-MAY-2002; 2002WO-US016555.
XX
PR   25-MAY-2001; 2001US-0293231P.
PR   07-NOV-2001; 2001US-0331037P.
XX
PA   (UYDU-) UNIV DUKE.
XX
PI   Sullenger BA,  Rusconi C;
XX
DR   WPI; 2003-140438/13.
XX
PT   Altering affinity of nucleic acid ligands for target molecules in a
PT   patient or reversing binding of labeled ligands to target tissues, by
PT   administering (to a patient receiving the ligand) a modulator that binds
PT   to ligand.
XX
PS   Claim 50; Page 74; 111pp; English.
XX
CC   The present invention relates to a method for altering the affinity of a
CC   nucleic acid ligand (e.g. an aptamer) for a target molecule in a patient
CC   or in vitro, or reversing the binding of the labelled ligand to a target
CC   tissue. The method comprises administering a modulator that binds to the
CC   ligand to a patient receiving the ligand, or contacting the ligand with
CC   the modulator under conditions such that the modulator binds to the
CC   ligand, and thus alters the affinity of the ligand for the target
CC   molecule. The method is useful for treating a number of disorders e.g.
CC   infection, autoimmunity, tumours, inflammatory proliferative diseases and
CC   hypoglycaemia. The present sequence is an oligonucleotide modulator,
CC   which targets FIXa aptamer 9.3t. FIXa aptamer binds to human coagulation
CC   Factor IXa and was used to illustrate the method of the invention. This
CC   oligonucleotide was found to be effective at reversing FIXa aptamer's
CC   anticoagulation activity in human plasma in vitro
XX
SQ   Sequence 18 BP; 5 A; 3 C; 7 G; 0 T; 3 U; 0 Other;

  Query Match             50.0%;  Score 17;  DB 7;  Length 18;
  Best Local Similarity   70.6%;  Pred. No. 4.3e+02;
  Matches   12;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          18 UAAUGCUGCCUCCCCAU 34
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Db          18 TAATGCTGCCTCCCCAT 2


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Job time : 122.8 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 9, 2004, 02:54:20 ; Search time 27.8667 Seconds
(without alignments)
677.093 Million cell updates/sec

Title: US-09-963-827B-70
Perfect score: 34
Sequence: 1 auggggacuauaccgcguaaugcugccuccccau 34

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 979464

Minimum DB seq length: 0
Maximum DB seq length: 200

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	17.2	50.6	115	4	US-09-621-976-13765	Sequence 13765, A
	2	17.2	50.6	196	4	US-09-643-597-317	Sequence 317, App
	3	17.2	50.6	196	4	US-09-480-884A-317	Sequence 317, App
	4	17.2	50.6	196	4	US-09-542-615A-317	Sequence 317, App
	5	17.2	50.6	196	4	US-09-606-421B-317	Sequence 317, App
	6	17	50.0	46	2	US-08-448-267A-6	Sequence 6, Appli
c	7	15.4	45.3	38	4	US-09-474-432B-1341	Sequence 1341, Ap
c	8	15.4	45.3	38	4	US-09-476-387-1340	Sequence 1340, Ap
	9	15.4	45.3	147	4	US-09-536-094-2	Sequence 2, Appli
c	10	15.4	45.3	183	4	US-09-134-001C-282	Sequence 282, App
	11	15	44.1	117	4	US-09-313-294A-6423	Sequence 6423, Ap
c	12	14.8	43.5	46	4	US-09-486-241-1	Sequence 1, Appli
	13	14.8	43.5	94	4	US-08-585-593A-18	Sequence 18, Appl
	14	14.8	43.5	130	4	US-08-956-171E-2661	Sequence 2661, Ap
	15	14.6	42.9	50	4	US-09-168-947-9	Sequence 9, Appli
c	16	14.6	42.9	71	4	US-08-956-171E-1721	Sequence 1721, Ap
c	17	14.6	42.9	76	4	US-09-025-769B-134	Sequence 134, App
	18	14.6	42.9	77	1	US-08-477-530-6	Sequence 6, Appli
	19	14.6	42.9	77	1	US-08-477-530-6	Sequence 6, Appli
	20	14.6	42.9	77	1	US-08-477-830-6	Sequence 6, Appli
	21	14.6	42.9	111	4	US-09-702-705-1556	Sequence 1556, Ap
	22	14.6	42.9	111	4	US-09-736-457-1556	Sequence 1556, Ap
	23	14.6	42.9	111	4	US-09-614-124B-1556	Sequence 1556, Ap
	24	14.6	42.9	111	4	US-09-671-325-1556	Sequence 1556, Ap
c	25	14.6	42.9	196	4	US-07-757-022B-21	Sequence 21, Appl
	26	14.4	42.4	29	4	US-09-304-232-17	Sequence 17, Appl
c	27	14.4	42.4	98	1	US-08-472-255A-12	Sequence 12, Appl
c	28	14.4	42.4	98	1	US-08-479-724A-12	Sequence 12, Appl
c	29	14.4	42.4	98	3	US-08-472-256B-12	Sequence 12, Appl
c	30	14.4	42.4	98	3	US-08-952-793-12	Sequence 12, Appl
c	31	14.4	42.4	98	4	US-09-849-928-12	Sequence 12, Appl
c	32	14.4	42.4	98	5	PCT-US96-09455A-12	Sequence 12, Appl
c	33	14.4	42.4	103	3	US-08-952-664-12	Sequence 12, Appl
c	34	14.4	42.4	103	3	US-09-487-874-12	Sequence 12, Appl
c	35	14.4	42.4	142	4	US-08-956-171E-4735	Sequence 4735, Ap
c	36	14.4	42.4	189	4	US-09-621-976-18097	Sequence 18097, A
	37	14.2	41.8	27	3	US-09-269-345-7	Sequence 7, Appli
c	38	14.2	41.8	32	1	US-08-616-133-25	Sequence 25, Appl
c	39	14.2	41.8	32	1	US-08-802-985-25	Sequence 25, Appl
	40	14.2	41.8	39	6	5256648-11	Patent No. 5256648
	41	14.2	41.8	45	3	US-08-675-566-34	Sequence 34, Appl
	42	14.2	41.8	51	4	US-09-443-199C-65	Sequence 65, Appl
c	43	14.2	41.8	60	3	US-09-023-228B-126	Sequence 126, App
c	44	14.2	41.8	60	4	US-09-163-025B-126	Sequence 126, App
c	45	14.2	41.8	60	4	US-10-037-282-126	Sequence 126, App

ALIGNMENTS

RESULT 1
US-09-621-976-13765
; Sequence 13765, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13765
; LENGTH: 115
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-13765

Query Match 50.6%; Score 17.2; DB 4; Length 115;
Best Local Similarity 56.7%; Pred. No. 75;
Matches 17; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

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Db         63 GGAGATTGGACGGCCTGATGCTCCCTCCCC 92
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RESULT 2
US-09-643-597-317
; Sequence 317, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21

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;  NUMBER OF SEQ ID NOS:  369
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 317
;   LENGTH: 196
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-643-597-317

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  Matches   17;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          3 GGGGACUAUACCGCGUAAUGCUGCCUCCCC 32
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Db        104 GGAGATTGGACGGCCTGATGCTCCCTCCCC 133


RESULT 3
US-09-480-884A-317
; Sequence 317, Application US/09480884A
; Patent No. 6482597
; GENERAL INFORMATION:
;  APPLICANT: Wang, Tongtong
;  APPLICANT:  Fan, Liqun
;  APPLICANT:  Hosken, Nancy A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.455C6
;  CURRENT APPLICATION NUMBER: US/09/480,884A
;  CURRENT FILING DATE:  2001-08-27
;  NUMBER OF SEQ ID NOS: 330
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 317
;   LENGTH: 196
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-480-884A-317

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  Best Local Similarity   56.7%;  Pred. No. 84;
  Matches   17;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          3 GGGGACUAUACCGCGUAAUGCUGCCUCCCC 32
              || ||  :  || ||  : |:||: ||:|||| 
Db        104 GGAGATTGGACGGCCTGATGCTCCCTCCCC 133


RESULT 4
US-09-542-615A-317
; Sequence 317, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Fan, Liqun
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Hosken, Nancy A.
;  APPLICANT:  Fanger, Gary R.
;  TITLE OF INVENTION:  COMPOUNDS AND METHODS FOR THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE:  210121.455C8
;  CURRENT APPLICATION NUMBER: US/09/542,615A
;  CURRENT FILING DATE:  2000-04-14
;  NUMBER OF SEQ ID NOS:  350
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 317
;   LENGTH: 196
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-542-615A-317

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Qy          3 GGGGACUAUACCGCGUAAUGCUGCCUCCCC 32
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Db        104 GGAGATTGGACGGCCTGATGCTCCCTCCCC 133


RESULT 5
US-09-606-421B-317
; Sequence 317, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
;  APPLICANT: Wang, Tongtong
;  APPLICANT:  Fan, Liqun
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Hosken, Nancy
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Li, Samuel X.
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.455C9
;  CURRENT APPLICATION NUMBER: US/09/606,421B
;  CURRENT FILING DATE:  2000-06-28
;  NUMBER OF SEQ ID NOS: 358
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 317
;   LENGTH: 196
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-606-421B-317

  Query Match             50.6%;  Score 17.2;  DB 4;  Length 196;
  Best Local Similarity   56.7%;  Pred. No. 84;
  Matches   17;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          3 GGGGACUAUACCGCGUAAUGCUGCCUCCCC 32
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Db        104 GGAGATTGGACGGCCTGATGCTCCCTCCCC 133


RESULT 6
US-08-448-267A-6
; Sequence 6, Application US/08448267A
; Patent No. 5925518
;  GENERAL INFORMATION:
;    APPLICANT:  Earle, Steven R.
;    APPLICANT:  Jacobson, Walter E.
;    TITLE OF INVENTION:  Nucleic Acid Primers for Amplification
;    TITLE OF INVENTION:  of a Mycobacteria RNA Template
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Akzo No. 5925518el Patent Department
;      STREET:  1300 Piccard Drive, Suite 206
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/448,267A
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gormley, Mary E.
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;      REGISTRATION NUMBER:  34,409
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  301-258-5200
;      TELEFAX:  301-977-0847
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  46 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "synthetic DNA primer"
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  5..21
;      OTHER INFORMATION:  /note= "T7 RNA polymerase promoter"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  25..46
;      OTHER INFORMATION:  /note= "hybridization region"
US-08-448-267A-6

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  Best Local Similarity  60.0%;  Pred. No. 77;
  Matches   15;  Conservative    5;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          7 ACUAUACCGCGUAAUGCUGCCUCCC 31
              |||:|  | | | :||:|||:|||
Db         16 ACTATAGGGAGAACTGCTGCCTCCC 40


RESULT 7
US-09-474-432B-1341/c
; Sequence 1341, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Beigelman, Leo
;  APPLICANT:  Burgin, Alex
;  APPLICANT:  Beaudry, Amber
;  APPLICANT:  Karpeisky, Alex
;  APPLICANT:  Adamic, Jasenka
;  APPLICANT:  Sweedler, David
;  APPLICANT:  Zinnen, Shawn
;  TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
;  FILE REFERENCE: MBHB00-831-B (247/276)
;  CURRENT APPLICATION NUMBER: US/09/474,432B
;  CURRENT FILING DATE:  1999-12-19
;  PRIOR APPLICATION NUMBER: US 60/064,866
;  PRIOR FILING DATE: 1997-11-05
;  PRIOR APPLICATION NUMBER: US 60/084,727
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: US 09/186,675
;  PRIOR FILING DATE: 1998-11-04
;  PRIOR APPLICATION NUMBER: US 09/301,511
;  PRIOR FILING DATE: 1999-04-28
;  NUMBER OF SEQ ID NOS: 1526
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1341
;   LENGTH: 38
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
US-09-474-432B-1341

  Query Match           45.3%;  Score 15.4;  DB 4;  Length 38;
  Best Local Similarity  51.5%;  Pred. No. 4e+02;
  Matches   17;  Conservative    5;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          2 UGGGGACUAUACCGCGUAAUGCUGCCUCCCCAU 34
              :|| |||  :  | ||   : | |||:|||||:
Db         33 TGGAGACCTTGACTCGCCTTTCGGCCTCCCCAT 1


RESULT 8
US-09-476-387-1340/c
; Sequence 1340, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Beigelman, Leo
;  APPLICANT:  Beaudry, Amber
;  APPLICANT:  Karpeisky, Alex
;  APPLICANT:  Adamic, Jasenka Matulic
;  APPLICANT:  Sweedler, Dave
;  APPLICANT:  Zinnen, Shawn
;  TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleot
;  FILE REFERENCE: MBHB00-831-C (249/073)
;  CURRENT APPLICATION NUMBER: US/09/476,387
;  CURRENT FILING DATE:  2001-04-04
;  PRIOR APPLICATION NUMBER: 09/474,432
;  PRIOR FILING DATE: 1999-12-29
;  PRIOR APPLICATION NUMBER: 09/301,511
;  PRIOR FILING DATE: 1999-04-28
;  PRIOR APPLICATION NUMBER: 09/186,675
;  PRIOR FILING DATE: 1998-11-04
;  PRIOR APPLICATION NUMBER: 60/083,727
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/064,866
;  PRIOR FILING DATE: 1997-11-05
;  NUMBER OF SEQ ID NOS: 1524
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1340
;   LENGTH: 38
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
US-09-476-387-1340

  Query Match           45.3%;  Score 15.4;  DB 4;  Length 38;
  Best Local Similarity  51.5%;  Pred. No. 4e+02;
  Matches   17;  Conservative    5;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          2 UGGGGACUAUACCGCGUAAUGCUGCCUCCCCAU 34
              :|| |||  :  | ||   : | |||:|||||:
Db         33 TGGAGACCTTGACTCGCCTTTCGGCCTCCCCAT 1


RESULT 9
US-09-536-094-2
; Sequence 2, Application US/09536094
; Patent No. 6303845
; GENERAL INFORMATION:
;  APPLICANT: Shen, Che-Kun James
;  TITLE OF INVENTION: HS-40 ENHANCER-CONTAINING VECTOR
;  FILE REFERENCE: 08919/016001
;  CURRENT APPLICATION NUMBER: US/09/536,094
;  CURRENT FILING DATE:  2000-03-24
;  PRIOR APPLICATION NUMBER: 09/205,015
;  PRIOR FILING DATE: 1998-12-04
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 147
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-536-094-2

  Query Match           45.3%;  Score 15.4;  DB 4;  Length 147;
  Best Local Similarity  45.5%;  Pred. No. 5.2e+02;
  Matches   15;  Conservative    7;  Mismatches   11;  Indels    0;  Gaps    0;
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Qy          2 UGGGGACUAUACCGCGUAAUGCUGCCUCCCCAU 34
              :|  || :| | |   :  :||:|||:|||| :
Db        104 TGCTGATTACAACCTCTGGTGCTGCCTCCCCCT 136


RESULT 10
US-09-134-001C-282/c
; Sequence 282, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
;  TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
;  CURRENT APPLICATION NUMBER: US/09/134,001C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/064,964
;  PRIOR FILING DATE: 1997-11-08
;  PRIOR APPLICATION NUMBER: US 60/055,779
;  PRIOR FILING DATE: 1997-08-14
;  NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 282
;   LENGTH: 183
;   TYPE: DNA
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-282

  Query Match            45.3%;  Score 15.4;  DB 4;  Length 183;
  Best Local Similarity  56.0%;  Pred. No. 5.5e+02;
  Matches   14;  Conservative    5;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          7 ACUAUACCGCGUAAUGCUGCCUCCC 31
              || |:||| ||:| :| :| |:| |
Db        177 ACAATACCTCGTATTGTTGGCTCGC 153


RESULT 11
US-09-313-294A-6423
; Sequence 6423, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
;  APPLICANT:  Lalgudi, Raghunath V.
;  APPLICANT:  Ito, Laura Y.
;  APPLICANT:  Sherman, Bradley K.
;  TITLE OF INVENTION:  POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
;  FILE REFERENCE:  PL-0017 US
;  CURRENT APPLICATION NUMBER: US/09/313,294A
;  CURRENT FILING DATE:  1999-05-14
;  NUMBER OF SEQ ID NOS:  7600
;  SOFTWARE:  PERL Program
; SEQ ID NO 6423
;   LENGTH: 117
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6476212 700351779H1
;   NAME/KEY: unsure
;   LOCATION: 31
;   OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-6423

  Query Match            44.1%;  Score 15;  DB 4;  Length 117;
  Best Local Similarity  50.0%;  Pred. No. 7.6e+02;
  Matches   16;  Conservative    5;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          3 GGGGACUAUACCGCGUAAUGCUGCCUCCCCAU 34
              |||| | |:|| |||:  : |:|    ||| :
Db          6 GGGGTCCATACGGCGTTGTTCTGGANTCCCGT 37


RESULT 12
US-09-486-241-1/c
; Sequence 1, Application US/09486241
; Patent No. 6472184
; GENERAL INFORMATION:
;  APPLICANT: Hegemann, Peter
;  TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEIC ACID
;  TITLE OF INVENTION:  POLYMERS
;  FILE REFERENCE: 3910/0G706
;  CURRENT APPLICATION NUMBER: US/09/486,241
;  CURRENT FILING DATE:  2000-02-22
;  PRIOR APPLICATION NUMBER: PCT/EP98/05219
;  PRIOR FILING DATE: 1998-08-17
;  PRIOR APPLICATION NUMBER: DE19736591.4
;  PRIOR FILING DATE: 1997-08-22
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 46
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
US-09-486-241-1

  Query Match            43.5%;  Score 14.8;  DB 4;  Length 46;
  Best Local Similarity  55.9%;  Pred. No. 7.8e+02;
  Matches   19;  Conservative    3;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 AUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAU 34
              |:|||||| | ||||    ||      ||:| || :
Db         41 ATGGGGACCACACCGGTGAACAGCTCCTCGCCCT 8


RESULT 13
US-08-585-593A-18
; Sequence 18, Application US/08585593A
; Patent No. 6503706
;  GENERAL INFORMATION:
;    APPLICANT:  ABKEN, Hinrich J
;    APPLICANT:  ALBERT, Winfried
;    APPLICANT:  JUNGFER, Herbert
;    TITLE OF INVENTION:  METHOD OF IDENTIFYING HUMAN AND ANIMAL
;    TITLE OF INVENTION:  CELLS CAPABLE OF UNLIMITED PROLIFERATION OR TUMOR
;    TITLE OF INVENTION:  FORMATION
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nikaido, Marmelstein, Murray & Oram LLP
;      STREET:  655 Fifteenth Street N.W. Suite 330
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-5701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/585,593A
;      FILING DATE:  16-JAN-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP94/02307
;      FILING DATE:  13-JUL-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P 43 23 727.4
;      FILING DATE:  15-JUL-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murray, Robert B.
;      REGISTRATION NUMBER:  22,980
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)638-5000
;      TELEFAX:  (202)638-4810
;  INFORMATION FOR SEQ ID NO:  18:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  94 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-585-593A-18

  Query Match             43.5%;  Score 14.8;  DB 4;  Length 94;
  Best Local Similarity   57.7%;  Pred. No. 9e+02;
  Matches   15;  Conservative    4;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          5 GGACUAUACCGCGUAAUGCUGCCUCC 30
              || |:  || | | ||: |:|||:||
Db         52 GGGCTGCACAGAGAAATCCTGCCTCC 77


RESULT 14
US-08-956-171E-2661
; Sequence 2661, Application US/08956171E
; Patent No. 6593114
;   GENERAL INFORMATION:
;        APPLICANT: Charles Kunsch
;                   Gil H. Choi
;                   Patrick S. Dillon
;                   Craig A. Rosen
;                   Steven C. Barash
;                   Michael R. Fannon
;        TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;        NUMBER OF SEQUENCES: 5256
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Human Genome Sciences, Inc.
;             STREET: 9410 Key West Avenue
;             CITY: Rockville
;             STATE: Maryland
;             COUNTRY: USA
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;             COMPUTER: HP Vectra 486/33
;             OPERATING SYSTEM: MSDOS version 6.2
;             SOFTWARE: ASCII Text
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/956,171E
;             FILING DATE: 20-Oct-1997
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/009,861
;             FILING DATE: January 5, 1996
;             APPLICATION NUMBER: 08/781,986
;             FILING DATE: January 3, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Mark J. Hyman
;             REGISTRATION NUMBER: 46,789
;             REFERENCE/DOCKET NUMBER: PB248P1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (240) 314-1224
;             TELEFAX: (301) 309-8439
;   INFORMATION FOR SEQ ID NO: 2661:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 130 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2661:
US-08-956-171E-2661

  Query Match             43.5%;  Score 14.8;  DB 4;  Length 130;
  Best Local Similarity   50.0%;  Pred. No. 9.6e+02;
  Matches   17;  Conservative    5;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 AUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAU 34
              |:||||    : ||||  ||: | |  :|||| :
Db         12 ATGGGGTAATTTCCGCCAAATCCCGTTTCCCCCT 45


RESULT 15
US-09-168-947-9
; Sequence 9, Application US/09168947
; Patent No. 6589734
; GENERAL INFORMATION:
;  APPLICANT: KACIAN, DANIEL L.
;  APPLICANT: FULTZ, TIMOTHY J.
;  APPLICANT: MCDONOUGH, SHERROL H.
;  TITLE OF INVENTION: DETECTION OF HIV
;  FILE REFERENCE: 218/130
;  CURRENT APPLICATION NUMBER: US/09/168,947
;  CURRENT FILING DATE: 1998-10-08
;  EARLIER APPLICATION NUMBER: 08/469,067
;  EARLIER FILING DATE: 1995-06-06
;  EARLIER APPLICATION NUMBER: 07/550,837
;  EARLIER FILING DATE: 1990-07-10
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthesized nucleic acid molecule
US-09-168-947-9

  Query Match             42.9%;  Score 14.6;  DB 4;  Length 50;
  Best Local Similarity   55.2%;  Pred. No. 9.8e+02;
  Matches   16;  Conservative    4;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 AUGGGGACUAUACCGCGUAAUGCUGCCUC 29
              | || |||:   |||| :||: |:| | |
Db         21 AGGGAGACTCCCCCGCTTAATACTGACGC 49


Search completed: April  9, 2004, 06:07:34
Job time : 29.8667 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 9, 2004, 03:53:35 ; Search time 420.8 Seconds
(without alignments)
303.112 Million cell updates/sec

Title: US-09-963-827B-70
Perfect score: 34
Sequence: 1 auggggacuauaccgcguaaugcugccuccccau 34

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2475585 seqs, 1875730760 residues

Total number of hits satisfying chosen parameters: 1817818

Minimum DB seq length: 0
Maximum DB seq length: 200

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	34	100.0	34	10	US-09-963-827B-70	Sequence 70, Appl
	2	34	100.0	35	14	US-10-155-233-1	Sequence 1, Appli
	3	34	100.0	35	14	US-10-155-233-19	Sequence 19, Appl
	4	34	100.0	40	14	US-10-155-233-2	Sequence 2, Appli
	5	34	100.0	96	10	US-09-963-827B-3	Sequence 3, Appli
c	6	21	61.8	23	14	US-10-155-233-29	Sequence 29, Appl
	7	17.2	50.6	196	9	US-09-735-705-317	Sequence 317, App
	8	17.2	50.6	196	9	US-09-850-716A-317	Sequence 317, App
	9	17.2	50.6	196	9	US-09-897-778-317	Sequence 317, App
	10	17.2	50.6	196	14	US-10-117-982-317	Sequence 317, App
	11	17.2	50.6	196	15	US-10-313-986-317	Sequence 317, App
c	12	17	50.0	17	14	US-10-155-233-25	Sequence 25, Appl
c	13	17	50.0	17	14	US-10-155-233-41	Sequence 41, Appl
c	14	17	50.0	18	14	US-10-155-233-26	Sequence 26, Appl
c	15	17	50.0	20	14	US-10-155-233-20	Sequence 20, Appl
c	16	17	50.0	112	9	US-09-864-761-22160	Sequence 22160, A
	17	16.6	48.8	66	15	US-10-027-632-178287	Sequence 178287,
	18	16.6	48.8	66	15	US-10-027-632-178299	Sequence 178299,
c	19	16.6	48.8	200	10	US-09-814-353-13516	Sequence 13516, A
	20	16.4	48.2	161	15	US-10-027-632-178667	Sequence 178667,
c	21	16.4	48.2	199	12	US-10-085-783A-15330	Sequence 15330, A
c	22	16.4	48.2	199	15	US-10-242-535A-15330	Sequence 15330, A
c	23	16.2	47.6	113	9	US-09-864-761-27147	Sequence 27147, A
	24	15.6	45.9	33	14	US-10-155-233-18	Sequence 18, Appl
	25	15.6	45.9	76	9	US-09-815-242-805	Sequence 805, App
	26	15.6	45.9	76	12	US-10-282-122A-775	Sequence 775, App
	27	15.6	45.9	164	9	US-09-864-761-18483	Sequence 18483, A
c	28	15.4	45.3	38	10	US-09-825-805-1340	Sequence 1340, Ap
c	29	15.4	45.3	64	10	US-09-766-880B-16	Sequence 16, Appl
	30	15.4	45.3	147	9	US-09-977-432-2	Sequence 2, Appli
	31	15.4	45.3	147	9	US-09-961-563-2	Sequence 2, Appli
	32	15.4	45.3	147	13	US-10-014-220-2	Sequence 2, Appli
c	33	15.4	45.3	162	12	US-10-085-783A-626	Sequence 626, App
c	34	15.4	45.3	162	15	US-10-242-535A-626	Sequence 626, App
	35	15.4	45.3	190	9	US-09-864-761-31632	Sequence 31632, A
	36	15.2	44.7	105	9	US-09-896-915-38	Sequence 38, Appl
c	37	15.2	44.7	121	10	US-09-818-875-1097	Sequence 1097, Ap
	38	15.2	44.7	121	10	US-09-818-875-1098	Sequence 1098, Ap
c	39	15.2	44.7	121	15	US-10-209-787-1097	Sequence 1097, Ap
	40	15.2	44.7	121	15	US-10-209-787-1098	Sequence 1098, Ap
c	41	15.2	44.7	121	15	US-10-261-185-1097	Sequence 1097, Ap
	42	15.2	44.7	121	15	US-10-261-185-1098	Sequence 1098, Ap
	43	15.2	44.7	130	12	US-10-424-599-30668	Sequence 30668, A
c	44	15.2	44.7	137	12	US-10-424-599-41653	Sequence 41653, A
	45	15.2	44.7	152	12	US-10-424-599-133545	Sequence 133545,

ALIGNMENTS

RESULT 1
US-09-963-827B-70
; Sequence 70, Application US/09963827B
; Publication No. US20030175703A1
; GENERAL INFORMATION:
; APPLICANT: Duke University
; APPLICANT: Sullenger, Bruce
; APPLICANT: Rusconi, Christopher
; TITLE OF INVENTION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME
; FILE REFERENCE: 180/124/2
; CURRENT APPLICATION NUMBER: US/09/963,827B
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,654
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 70
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: RNA aptamer
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(34)
; OTHER INFORMATION: RNA aptamer
US-09-963-827B-70

Query Match 100.0%; Score 34; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAU 34
              ||||||||||||||||||||||||||||||||||
Db          1 AUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAU 34
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RESULT 2

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US-10-155-233-1
; Sequence 1, Application US/10155233
; Publication No. US20030083294A1
; GENERAL INFORMATION:
;  APPLICANT: SULLENGER, BRUCE A
;  APPLICANT:  RUSCONI, CHRISTOPHER
;  TITLE OF INVENTION: MODULATORS OF PHARMACOLOGICAL AGENTS
;  FILE REFERENCE: 1579-684
;  CURRENT APPLICATION NUMBER: US/10/155,233
;  CURRENT FILING DATE:  2002-05-28
;  PRIOR APPLICATION NUMBER: 60/293,231
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/331,037
;  PRIOR FILING DATE: 2001-11-07
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 35
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Aptamer
;   FEATURE:
;   NAME/KEY: misc_RNA
;   LOCATION: (35)
;   OTHER INFORMATION: N=idT
US-10-155-233-1

  Query Match            100.0%;  Score 34;  DB 14;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-06;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUGGGGACUAUACCGCGUAAUGCUGCCUCCCCCAU 34
              ||||||||||||||||||||||||||||||||||
Db          1 AUGGGGACUAUACCGCGUAAUGCUGCCUCCCCCAU 34


RESULT 3
US-10-155-233-19
; Sequence 19, Application US/10155233
; Publication No. US20030083294A1
; GENERAL INFORMATION:
;  APPLICANT: SULLENGER, BRUCE A
;  APPLICANT:  RUSCONI, CHRISTOPHER
;  TITLE OF INVENTION: MODULATORS OF PHARMACOLOGICAL AGENTS
;  FILE REFERENCE: 1579-684
;  CURRENT APPLICATION NUMBER: US/10/155,233
;  CURRENT FILING DATE:  2002-05-28
;  PRIOR APPLICATION NUMBER: 60/293,231
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/331,037
;  PRIOR FILING DATE: 2001-11-07
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
;   LENGTH: 35
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Aptamer
;   FEATURE:
;   NAME/KEY: misc_RNA
;   LOCATION: (27)
;   OTHER INFORMATION: N=mGmUmCidT
US-10-155-233-19

  Query Match            100.0%;  Score 34;  DB 14;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-06;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUGGGGACUAUACCGCGUAAUGCUGCCUCCCCCAU 34
              ||||||||||||||||||||||||||||||||||
Db          1 AUGGGGACUAUACCGCGUAAUGCUGCCUCCCCCAU 34


RESULT 4
US-10-155-233-2
; Sequence 2, Application US/10155233
; Publication No. US20030083294A1
; GENERAL INFORMATION:
;  APPLICANT: SULLENGER, BRUCE A
;  APPLICANT:  RUSCONI, CHRISTOPHER
;  TITLE OF INVENTION: MODULATORS OF PHARMACOLOGICAL AGENTS
;  FILE REFERENCE: 1579-684
;  CURRENT APPLICATION NUMBER: US/10/155,233
;  CURRENT FILING DATE:  2002-05-28
;  PRIOR APPLICATION NUMBER: 60/293,231
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/331,037
;  PRIOR FILING DATE: 2001-11-07
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 40
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Aptamer
US-10-155-233-2

  Query Match            100.0%;  Score 34;  DB 14;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-06;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUGGGGACUAUACCGCGUAAUGCUGCCUCCCCCAU 34
              ||||||||||||||||||||||||||||||||||
Db          4 AUGGGGACUAUACCGCGUAAUGCUGCCUCCCCCAU 37


RESULT 5
US-09-963-827B-3
; Sequence 3, Application US/09963827B
; Publication No. US20030175703A1
; GENERAL INFORMATION:
;  APPLICANT: Duke University
;  APPLICANT:  Sullenger, Bruce
;  APPLICANT:  Rusconi, Christopher
;  TITLE OF INVENTION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME
;  FILE REFERENCE: 180/124/2
;  CURRENT APPLICATION NUMBER: US/09/963,827B
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 60/235,654
;  PRIOR FILING DATE: 2000-09-26
;  NUMBER OF SEQ ID NOS: 227
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 96
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: RNA aptamer
;   FEATURE:
;   NAME/KEY: RNA aptamer
;   LOCATION: (1)..(96)
;   OTHER INFORMATION: RNA aptamer
US-09-963-827B-3

  Query Match            100.0%;  Score 34;  DB 10;  Length 96;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-06;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUGGGGACUAUACCGCGUAAUGCUGCCUCCCCCAU 34
              ||||||||||||||||||||||||||||||||||
Db         18 AUGGGGACUAUACCGCGUAAUGCUGCCUCCCCCAU 51
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RESULT 6
US-10-155-233-29/c
; Sequence 29, Application US/10155233
; Publication No. US20030083294A1
; GENERAL INFORMATION:
;  APPLICANT: SULLENGER, BRUCE A
;  APPLICANT:  RUSCONI, CHRISTOPHER
;  TITLE OF INVENTION: MODULATORS OF PHARMACOLOGICAL AGENTS
;  FILE REFERENCE: 1579-684
;  CURRENT APPLICATION NUMBER: US/10/155,233
;  CURRENT FILING DATE:  2002-05-28
;  PRIOR APPLICATION NUMBER: 60/293,231
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/331,037
;  PRIOR FILING DATE: 2001-11-07
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
;   LENGTH: 23
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Aptamer
US-10-155-233-29

  Query Match             61.8%;  Score 21;  DB 14;  Length 23;
  Best Local Similarity   81.0%;  Pred. No. 6.4;
  Matches   17;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GGGGACUAUACCGCGUAAUGC 23
              ||||||:|:||||||:||:||
Db         21 GGGGACTATACCGCGTAATGC 1


RESULT 7
US-09-735-705-317
; Sequence 317, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Fan, Liqun
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Hosken, Nancy
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Li, Samuel X.
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Fanger, Neil
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE:  210121.455C14
;  CURRENT APPLICATION NUMBER: US/09/735,705
;  CURRENT FILING DATE:  2000-12-12
;  NUMBER OF SEQ ID NOS:  419
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 317
;   LENGTH: 196
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-735-705-317

  Query Match             50.6%;  Score 17.2;  DB 9;  Length 196;
  Best Local Similarity   56.7%;  Pred. No. 4.6e+02;
  Matches   17;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          3 GGGGACUAUACCGCGUAAUGCUGCCUCCCC 32
              || || :  || || : |:||: ||:||||
Db        104 GGAGATTGGACGGCCTGATGCTCCCTCCCC 133


RESULT 8
US-09-850-716A-317
; Sequence 317, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
;  APPLICANT: Kalos, Michael D.
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Retter, Marc W.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.455C15
;  CURRENT APPLICATION NUMBER: US/09/850,716A
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 440
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 317
;   LENGTH: 196
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-850-716A-317

  Query Match             50.6%;  Score 17.2;  DB 9;  Length 196;
  Best Local Similarity   56.7%;  Pred. No. 4.6e+02;
  Matches   17;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          3 GGGGACUAUACCGCGUAAUGCUGCCUCCCC 32
              || || :  || || : |:||: ||:||||
Db        104 GGAGATTGGACGGCCTGATGCTCCCTCCCC 133


RESULT 9
US-09-897-778-317
; Sequence 317, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Tongtong
;  APPLICANT:  Marnerakis, Margarita
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Watanabe, Yoshihiro
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Peckham, David W.
;  APPLICANT:  Fanger, Neil
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.455C16
;  CURRENT APPLICATION NUMBER: US/09/897,778
;  CURRENT FILING DATE:  2001-06-28
;  NUMBER OF SEQ ID NOS: 467
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 317
;   LENGTH: 196
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-897-778-317

  Query Match             50.6%;  Score 17.2;  DB 9;  Length 196;
  Best Local Similarity   56.7%;  Pred. No. 4.6e+02;
  Matches   17;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          3 GGGGACUAUACCGCGUAAUGCUGCCUCCCC 32
              || || :  || || : |:||: ||:||||
Db        104 GGAGATTGGACGGCCTGATGCTCCCTCCCC 133


RESULT 10
US-10-117-982-317
; Sequence 317, Application US/10117982
; Publication No. US20030138438A1
; GENERAL INFORMATION:
;  APPLICANT: Foy, Teresa M.
;  APPLICANT:  Fanger, Gary R.
```

```
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Watanabe, Yoshihiro
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Mericle, Barbara
;  APPLICANT:  Spies, Gregory A.
;  APPLICANT:  Fan, Liqun
;  APPLICANT:  Wang, Tongtong
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.455C18
;  CURRENT APPLICATION NUMBER: US/10/117,982
;  CURRENT FILING DATE:  2002-04-05
;  NUMBER OF SEQ ID NOS: 484
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 317
;   LENGTH: 196
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-117-982-317

  Query Match             50.6%;  Score 17.2;  DB 14;  Length 196;
  Best Local Similarity   56.7%;  Pred. No. 4.6e+02;
  Matches   17;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          3 GGGGACUAUACCGCGUAAUGCUGCCUCCCC 32
              || ||  :  || ||  : |:||: ||:|||| 
Db        104 GGAGATTGGACGGCCTGATGCTCCCTCCCC 133


RESULT 11
US-10-313-986-317
; Sequence 317, Application US/10313986
; Publication No. US20030236209A1
; GENERAL INFORMATION:
;  APPLICANT: Foy, Teresa M.
;  APPLICANT:  McNabb, Andria
;  APPLICANT:  Watanabe, Yoshihiro
;  APPLICANT:  Reed, Steven G.
;  APPLICANT:  Wang, Tongtong
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.455C19
;  CURRENT APPLICATION NUMBER: US/10/313,986
;  CURRENT FILING DATE:  2002-12-04
;  NUMBER OF SEQ ID NOS: 560
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 317
;   LENGTH: 196
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-313-986-317

  Query Match             50.6%;  Score 17.2;  DB 15;  Length 196;
  Best Local Similarity   56.7%;  Pred. No. 4.6e+02;
  Matches   17;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          3 GGGGACUAUACCGCGUAAUGCUGCCUCCCC 32
              || ||  :  || ||  : |:||: ||:|||| 
Db        104 GGAGATTGGACGGCCTGATGCTCCCTCCCC 133


RESULT 12
US-10-155-233-25/c
; Sequence 25, Application US/10155233
; Publication No. US20030083294A1
; GENERAL INFORMATION:
;  APPLICANT: SULLENGER, BRUCE A
;  APPLICANT:  RUSCONI, CHRISTOPHER
;  TITLE OF INVENTION: MODULATORS OF PHARMACOLOGICAL AGENTS
;  FILE REFERENCE: 1579-684
;  CURRENT APPLICATION NUMBER: US/10/155,233
;  CURRENT FILING DATE:  2002-05-28
;  PRIOR APPLICATION NUMBER: 60/293,231
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/331,037
;  PRIOR FILING DATE: 2001-11-07
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Aptamer
US-10-155-233-25

  Query Match             50.0%;  Score 17;  DB 14;  Length 17;
  Best Local Similarity   70.6%;  Pred. No. 4.3e+02;
  Matches   12;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         18 UAAUGCUGCCUCCCCAU 34
              :||:||:|||:|||||: 
Db         17 TAATGCTGCCTCCCCAT 1


RESULT 13
US-10-155-233-41/c
; Sequence 41, Application US/10155233
; Publication No. US20030083294A1
; GENERAL INFORMATION:
;  APPLICANT: SULLENGER, BRUCE A
;  APPLICANT:  RUSCONI, CHRISTOPHER
;  TITLE OF INVENTION: MODULATORS OF PHARMACOLOGICAL AGENTS
;  FILE REFERENCE: 1579-684
;  CURRENT APPLICATION NUMBER: US/10/155,233
;  CURRENT FILING DATE:  2002-05-28
;  PRIOR APPLICATION NUMBER: 60/293,231
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/331,037
;  PRIOR FILING DATE: 2001-11-07
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Aptamer
US-10-155-233-41

  Query Match             50.0%;  Score 17;  DB 14;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 4.3e+02;
  Matches   14;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUGGGGACUAUACCGCG 17
              |:||||||:|:|||||| 
Db         17 ATGGGGACTATACCGCG 1


RESULT 14
US-10-155-233-26/c
; Sequence 26, Application US/10155233
; Publication No. US20030083294A1
; GENERAL INFORMATION:
;  APPLICANT: SULLENGER, BRUCE A
;  APPLICANT:  RUSCONI, CHRISTOPHER
;  TITLE OF INVENTION: MODULATORS OF PHARMACOLOGICAL AGENTS
;  FILE REFERENCE: 1579-684
;  CURRENT APPLICATION NUMBER: US/10/155,233
;  CURRENT FILING DATE:  2002-05-28
;  PRIOR APPLICATION NUMBER: 60/293,231
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/331,037
;  PRIOR FILING DATE: 2001-11-07
```

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;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
;   LENGTH: 18
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Aptamer
US-10-155-233-26

  Query Match             50.0%;  Score 17;  DB 14;  Length 18;
  Best Local Similarity   70.6%;  Pred. No. 4.3e+02;
  Matches   12;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         18 UAAUGCUGCCUCCCCAU 34
              :||:||:|||:|||||:
Db         18 TAATGCTGCCTCCCCAT 2


RESULT 15
US-10-155-233-20/c
; Sequence 20, Application US/10155233
; Publication No. US20030083294A1
; GENERAL INFORMATION:
;  APPLICANT: SULLENGER, BRUCE A
;  APPLICANT:  RUSCONI, CHRISTOPHER
;  TITLE OF INVENTION: MODULATORS OF PHARMACOLOGICAL AGENTS
;  FILE REFERENCE: 1579-684
;  CURRENT APPLICATION NUMBER: US/10/155,233
;  CURRENT FILING DATE:  2002-05-28
;  PRIOR APPLICATION NUMBER: 60/293,231
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/331,037
;  PRIOR FILING DATE: 2001-11-07
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
;   LENGTH: 20
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Aptamer
US-10-155-233-20

  Query Match             50.0%;  Score 17;  DB 14;  Length 20;
  Best Local Similarity   70.6%;  Pred. No. 4.4e+02;
  Matches   12;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         18 UAAUGCUGCCUCCCCAU 34
              :||:||:|||:|||||:
Db         20 TAATGCTGCCTCCCCAT 4


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Title: US-09-963-827B-70
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

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Maximum Match 100%
Listing first 45 summaries

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25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		19.4	57.1	108	29	CG733695	CG733695 1119158F0
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3		18.8	55.3	179	10	BE183096	BE183096 CM2-HT065
	c 4	18.8	55.3	188	10	AW997328	AW997328 RC2-BN004
	c 5	18.6	54.7	145	9	AI873178	AI873178 wc47f02.x
	c 6	18.6	54.7	175	12	BI781660	BI781660 kh15d01.y
7		18	52.9	92	13	BU648134	BU648134 1112066D1
8		18	52.9	175	9	AA249214	AA249214 hfe0270.s
	c 9	17.8	52.4	194	9	AV011213	AV011213 AV011213
	c 10	17.6	51.8	119	28	AZ258888	AZ258888 RPCI-23-1
11		17.6	51.8	127	28	AZ121703	AZ121703 RPCI-23-4
12		17.6	51.8	168	10	BB170705	BB170705 BB170705
13		17.4	51.2	97	29	CG613410	CG613410 OST300555
14		17.4	51.2	160	14	CK296959	CK296959 EST759673
	c 15	17.2	50.6	56	28	AZ512563	AZ512563 1M0358G13
16		17.2	50.6	80	13	BQ818470	BQ818470 1030071B0
	c 17	17.2	50.6	107	13	BQ319143	BQ319143 PM4-CT056
18		17.2	50.6	111	13	BQ824632	BQ824632 1030120B0
19		17.2	50.6	138	12	BI998642	BI998642 1031060A1
20		17.2	50.6	143	12	BI022472	BI022472 CM3-MT034
21		17.2	50.6	149	9	AV390541	AV390541 AV390541
22		17.2	50.6	155	13	BQ808240	BQ808240 1030002G0
23		17.2	50.6	160	13	BQ824080	BQ824080 1030115F0
24		17.2	50.6	161	13	BQ822227	BQ822227 1030099C0
25		17.2	50.6	162	12	BI996058	BI996058 1031032H0
26		17.2	50.6	162	13	BQ824649	BQ824649 1030120C0
	c 27	17.2	50.6	163	10	AW146518	AW146518 ME000480.
28		17.2	50.6	163	13	BQ809459	BQ809459 1030011C0
29		17.2	50.6	172	12	BI997268	BI997268 1031048F0
30		17.2	50.6	175	13	BQ811695	BQ811695 1030025A0
31		17.2	50.6	177	13	BQ824879	BQ824879 1030122A0
32		17.2	50.6	178	12	BI720254	BI720254 1031048F0
33		17.2	50.6	185	12	BI816617	BI816617 1031063A1
	c 34	17.2	50.6	187	28	AZ372216	AZ372216 1M0124A05
35		17.2	50.6	188	28	BZ970131	BZ970131 PUGGX38TB
36		17.2	50.6	196	13	BQ825311	BQ825311 1030125H0
37		17.2	50.6	199	13	BQ821049	BQ821049 1030088H1
38		17	50.0	107	14	CF296285	CF296285 30DGS--06
	c 39	17	50.0	165	28	AQ304066	AQ304066 HS_3211_B
	c 40	17	50.0	188	28	BH086749	BH086749 RPCI-24-3
41		16.8	49.4	181	10	BF914058	BF914058 RC1-UT008
42		16.8	49.4	181	12	BM846477	BM846477 K-EST0125
43		16.8	49.4	196	10	BF956024	BF956024 RC3-NN118
44		16.6	48.8	85	9	AI001002	AI001002 os46g11.s
	c 45	16.6	48.8	102	12	BI039685	BI039685 IL3-NT028

ALIGNMENTS

RESULT 1
CG733695
LOCUS CG733695 108 bp DNA linear GSS 20-OCT-2003
DEFINITION 1119158F02.2EL_x1 1119 - RescueMu Grid AA Zea mays genomic, genomic survey sequence.
ACCESSION CG733695
VERSION CG733695.1 GI:37776187
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 108)
AUTHORS Walbot,V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1119158 row: 8

Class: transposon-tagged.

FEATURES Location/Qualifiers
source 1. .108
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 57.1%; Score 19.4; DB 29; Length 108;
Best Local Similarity 65.5%; Pred. No. 9.7e+02;
Matches 19; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 5 GGACUAUACCGCGUAAUGCUGCCUCCCCA 33
| ||: :|||||| |:||:||| || ||
Db 8 GAACTCTACCGCGCCATGCTGCCGCCTCA 36

RESULT 2
CG733696
LOCUS CG733696 108 bp DNA linear GSS 20-OCT-2003
DEFINITION 1119158F02.y1 1119 - RescueMu Grid AA Zea mays genomic, genomic survey sequence.
ACCESSION CG733696
VERSION CG733696.1 GI:37776188
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 108)
AUTHORS Walbot,V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site so sequence was trimmed. Post-ligation sequence submitted separately.
Plate: 1119158 row: 8
Class: transposon-tagged.

FEATURES Location/Qualifiers
source 1. .108
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 57.1%; Score 19.4; DB 29; Length 108;
Best Local Similarity 65.5%; Pred. No. 9.7e+02;
Matches 19; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 5 GGACUAUACCGCGUAAUGCUGCCUCCCCA 33
| ||: :|||||| |:||:||| || ||
Db 8 GAACTCTACCGCGCCATGCTGCCGCCTCA 36

RESULT 3
BE183096
LOCUS BE183096 179 bp mRNA linear EST 22-JUN-2000
DEFINITION CM2-HT0655-170400-157-h05 HT0655 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE183096
VERSION BE183096.1 GI:8662272
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 179)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=CM2-HT0655-170400-157-h05&t3=2000-04-17&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 36
High quality sequence stop: 178.

FEATURES Location/Qualifiers
source 1. .179
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0655"
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under

low stringency conditions."
ORIGIN

Query Match 55.3%; Score 18.8; DB 10; Length 179;
Best Local Similarity 56.7%; Pred. No. 2e+03;
Matches 17; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

```
Qy          2 UGGGGACUAUACCGCGUAAUGCUGCCUCCC 31
              :||| ||: : |||||   :||:|||: ||
Db         61 TGGGTACTTTGCCGCGCCGTGCTGCCTTCC 90
```

RESULT 4
AW997328/c
LOCUS AW997328 188 bp mRNA linear EST 05-JUN-2000
DEFINITION RC2-BN0048-250400-019-h08 BN0048 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW997328
VERSION AW997328.1 GI:8257562
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 188)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=RC2-BN0048-250400-019-h08&t3=2000-04-25&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 7
High quality sequence stop: 188.
FEATURES Location/Qualifiers
source 1. .188
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BN0048"
/note="Organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
ORIGIN

Query Match 55.3%; Score 18.8; DB 10; Length 188;
Best Local Similarity 63.3%; Pred. No. 2e+03;
Matches 19; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

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Qy          4 GGGACUAUACCGCGUAAUGCUGCCUCCCCA 33
              |||||  :||| ||   :||:|||:| |||
Db         57 GGGACCGTACCACGGTCTGCTGCCTCACCA 28
```

RESULT 5
AI873178/c
LOCUS AI873178 145 bp mRNA linear EST 17-DEC-1999
DEFINITION wc47f02.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2321787 3', mRNA sequence.
ACCESSION AI873178
VERSION AI873178.1 GI:5547227
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 145)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 760 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 142.
FEATURES Location/Qualifiers
source 1. .145
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2321787"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pr28"
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Pr22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo. "
ORIGIN

Query Match 54.7%; Score 18.6; DB 9; Length 145;
Best Local Similarity 54.5%; Pred. No. 2.3e+03;
Matches 18; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

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Qy          1 AUGGGGACUAUACCGCGUAAUGCUGCCUCCCCA 33
              |:| ||| : : ||| |: |:|  | |:|||||
Db         44 ATGCGGAATCTGCCGAGTGATGGCGGCTCCCCA 12
```

RESULT 6
BI781660/c
LOCUS BI781660 175 bp mRNA linear EST 26-SEP-2001
DEFINITION kh15d01.y1 Ascaris suum female gonad MZ pAMP1 v2 Chiapelli McCarter Ascaris suum cDNA 5', mRNA sequence.
ACCESSION BI781660
VERSION BI781660.1 GI:15784552
KEYWORDS EST.
SOURCE Ascaris suum (pig roundworm)
ORGANISM Ascaris suum
Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida;

```
            Ascaridoidea; Ascarididae; Ascaris.
REFERENCE   1  (bases 1 to 175)
  AUTHORS   McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
            Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,
            Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,
            Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
            Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,
            Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
            McCann,R., Waterston,R. and Wilson,R.
  TITLE     The Washington Univ. Nematode EST Project, 1999
  JOURNAL   Unpublished (1999)
COMMENT     Contact: McCarter JP
            The Washington Univ. Nematode EST Project, 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            The library was constructed by Brandi Chiapelli and Dr. James
            McCarter at Washington University, St. Louis. The cDNA was made by
            using Dynabead oligo-dT priming (Dynal). PCR based library using a
            modified protocol from the SMART PCR cDNA Synthesis Kit from
            Clontech. Directionally cloned into the UDG sites of pAMP1.
            Dissected nematode tissues were provided by Dr. Alan Scott
            (ascott@jhsph.edu). of the School of Public Hygene and Public Health
            at John Hopkins University in Baltimore, MD.
            Seq primer: -40RP from Gibco
            High quality sequence stop: 156.
FEATURES                Location/Qualifiers
     source             1. .175
                        /organism="Ascaris suum"
                        /mol_type="mRNA"
                        /db_xref="taxon:6253"
                        /sex="Female"
                        /tissue_type="Dissected female gonad (MZ=maturation zone,
                        most proximal region of gonad)"
                        /dev_stage="Adult"
                        /lab_host="DH10B"
                        /clone_lib="Ascaris suum female gonad MZ pAMP1 v2
                        Chiapelli McCarter"
                        /note="Vector: pAMP1 (Gibco); Site_1: NotI; Site_2: SalI;
                        The library was constructed by Brandi Chiapelli and Dr.
                        James McCarter at Washington University, St. Louis. The
                        cDNA was made by using Dynabead oligo-dT priming (Dynal).
                        PCR based library using a modified protocol from the SMART
                        PCR cDNA Synthesis Kit from Clontech. Directionally cloned
                        into the UDG sites of pAMP1. Dissected nematode tissues
                        were provided by Dr. Alan Scott (ascott@jhsph.edu) of the
                        School of Public Hygene and Public Health at John Hopkins
                        University in Baltimore, MD."
ORIGIN

  Query Match             54.7%;  Score 18.6;  DB 12;  Length 175;
  Best Local Similarity   51.5%;  Pred. No. 2.4e+03;
  Matches   17;  Conservative    7;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          2 UGGGGACUAUACCGCGUAAUGCUGCCUCCCCAU 34
              :||| | : : |||||   :||:|||: ||| :
Db        131 TGGGTAATTTGCCGCGCCTTGCTGCCTTCCCTT 99


RESULT 7
BU648134
LOCUS       BU648134                92 bp    mRNA    linear   EST 30-SEP-2002
DEFINITION  1112066D10.x1 C. reinhardtii CC-1690 (mt+), CC-1691 (mt-), Gamete
            (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA
            sequence.
ACCESSION   BU648134
VERSION     BU648134.1  GI:23360314
KEYWORDS    EST.
SOURCE      Chlamydomonas reinhardtii
  ORGANISM  Chlamydomonas reinhardtii
            Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
            Chlamydomonadaceae; Chlamydomonas.
REFERENCE   1  (bases 1 to 92)
  AUTHORS   Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C.,
            Lefebvre,P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D.
  TITLE     Analyses of the Chlamydomonas reinhardtii Genome: A Model,
            Unicellular System for Analyzing Gene Function and Regulation in
            Vascular Plants. Project: 1112
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Charles Hauser
            DCMB Box 91000
            Duke University
            Durham, NC 27708-1000
            Tel: 919 613 8159
            Fax: 919 613 8177
            Email: chauser@duke.edu.
FEATURES                Location/Qualifiers
     source             1. .92
                        /organism="Chlamydomonas reinhardtii"
                        /mol_type="mRNA"
                        /strain="21gr (CC-1690 wild type mt+) & 6145c (CC-1691
                        wild type mt-)"
                        /db_xref="taxon:3055"
                        /clone_lib="C. reinhardtii CC-1690 (mt+), CC-1691 (mt-),
                        Gamete (normalized), Lambda Zap II"
                        /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
                        XhoI; Gamete library was constructed by Hui Zhao, Min Lu,
                        Jeffrey McDermott, William J. Snell and John Davies.
                        Strain 21gr cells (CC-1690; mating type plus) and strain
                        6145c cells(CC-1691; mating type minus) that had been
                        growing on a light-dark cycle (13:11 L/D) in R-medium
                        (Sager and Granick) were separately transfered into
                        nitrogen-free medium at 8 hours into the light period.
                        PolyA mRNA was purified from each sample every 2 hours for
                        the next 18 hours. The mRNA was pooled and used for cDNA
                        synthesis. The cDNA was directionally cloned into lambda
                        Zap II (Stratagene) in the EcoRI (5') and XhoRI (3')
                        sites. pBluescript II SK- plasmids were excised from the
                        lambda ZAP clones by superinfection with ExAssist
                        (Stratagene) phage. The library was normalized using
                        method 4 described in Bonaldo et al., (1996) Genome
                        Research 6: 791-806."
ORIGIN

  Query Match             52.9%;  Score 18;  DB 13;  Length 92;
  Best Local Similarity   60.0%;  Pred. No. 3.6e+03;
  Matches   18;  Conservative    3;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          3 GGGGACUAUACCGCGUAAUGCUGCCUCCCC 32
              ||| || |  ||  |   :||:|||:||||
Db         48 GGGCACAACNCCCGGNNNTGCTGCCTCCCC 77


RESULT 8
AA249214
LOCUS       AA249214                175 bp    mRNA    linear   EST 11-MAR-1997
DEFINITION  hfe0270.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens
            cDNA 5', mRNA sequence.
ACCESSION   AA249214
VERSION     AA249214.1  GI:1879871
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 175)
  AUTHORS   Liew,C.C.
  TITLE     cDNAs from human fetal heart (1997)
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Liew CC
            Brigham and Women's Hospital
            Harvard Medical School
            75 Francis St. Boston, MA 02115, USA
            Tel: 6177328915
```

```
            Fax: 6179750995
            Email: cliew@rics.bwh.harvard.edu
            PCR PRimers
            FORWARD: 5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG 3'
            BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGGCG 3'
            Seq primer: 5' GAAATTAACCCTCACTAAAGGG 3'.
FEATURES              Location/Qualifiers
     source           1. .175
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /lab_host="E. coli XL1-Blue"
                      /clone_lib="Human fetal heart, Lambda ZAP Express"
                      /note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
                      XhoI; mRNA was purified from human fetal hearts (8-10
                      weeks). cDNA was synthesized using a XhoI-Oligo dT
                      adaptor-primer. EcoRI adaptors were ligated, followed by
                      digestion with XhoI, for directional cloning into
                      predigested lambda ZAP Express."
ORIGIN

  Query Match             52.9%;  Score 18;  DB 9;  Length 175;
  Best Local Similarity   50.0%;  Pred. No. 4.3e+03;
  Matches   17;  Conservative    7;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 AUGGGGACUAUACCGCGUAAUGCUGCCUCCCCCAU 34
              |:|||| | |:|| |||:  : |:|  : ||| :
Db          7 ATGGGGTCCATACGGCGTTGTTCTGGATTCCCGT 40


RESULT 9
AV011213/c
LOCUS       AV011213                194 bp    mRNA    linear   EST 25-AUG-1999
DEFINITION  AV011213 Mus musculus 18-day embryo C57BL/6J Mus musculus cDNA
            clone 1110030P07, mRNA sequence.
ACCESSION   AV011213
VERSION     AV011213.1  GI:4788200
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 194)
  AUTHORS   Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
            Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T.,
            Hara,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M.,
            Kawai,J., Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H.,
            Owa,C., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y.,
            Sugahara,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y.,
            Tominaga,N., Watanabe,S., Yagame,M., Yamamura,T., Yokota,T.,
            Yoshino,M., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Chie Owa
            Genome Science Laboratory
            RIKEN
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: 81-298-36-9145
            Fax: 81-298-36-9098
            Email: genome-res@rtc.riken.go.jp
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length cDNA
            (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
            Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
            Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES              Location/Qualifiers
     source           1. .194
                      /organism="Mus musculus"
                      /mol_type="mRNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="1110030P07"
                      /sex="mixed"
                      /dev_stage="18-day embryo"
                      /clone_lib="Mus musculus 18-day embryo C57BL/6J"
ORIGIN

  Query Match             52.4%;  Score 17.8;  DB 9;  Length 194;
  Best Local Similarity   58.6%;  Pred. No. 5.4e+03;
  Matches   17;  Conservative    5;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          5 GGACUAUACCGCGUAAUGCUGCCUCCCCA 33
              ||| : :| | || ||:||:  |:|||||
Db         63 GGAATTTATCCCGAAATGCTTGCTCCCCA 35


RESULT 10
AZ258888/c
LOCUS       AZ258888                119 bp    DNA     linear   GSS 26-JUL-2000
DEFINITION  RPCI-23-112I1.TV RPCI-23 Mus musculus genomic clone RPCI-23-112I1,
            genomic survey sequence.
ACCESSION   AZ258888
VERSION     AZ258888.1  GI:9464812
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 119)
  AUTHORS   Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,
            Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de
            Jong,P. and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-23
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: RPCI-23-112I1.TJ
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-23. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
            or from Resea ch Genetics (info@resgen.com). BAC end page:
            http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 112  row: I  column: 1
            Seq primer: T7
            Class: BAC ends.
FEATURES              Location/Qualifiers
     source           1. .119
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="RPCI-23-112I1"
                      /sex="Female"
                      /lab_host="DH10B"
                      /clone_lib="RPCI-23"
                      /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
                      EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
                      brain genomic DNA was isolated and partially digested
                      with a combination of EcoRI and EcoRI Methylase. Size
                      selected DNA was cloned into the pBACe3.6 vector at the
                      EcoRI sites. The ligation products were transformed into
                      DH10B electrocompetent cells (BRL Life Technologies). "
ORIGIN

  Query Match             51.8%;  Score 17.6;  DB 28;  Length 119;
  Best Local Similarity   53.1%;  Pred. No. 5.7e+03;
  Matches   17;  Conservative    6;  Mismatches    9;  Indels    0;  Gaps    0;
```

```
Qy          2 UGGGGACUAUACCGCGUAAUGCUGCCUCCCCA 33
              :||||||: :|| ||    :||:|| : | ||
Db         63 TGGGGACTTTACAGCTCTCTGCTGCTTACTCA 32


RESULT 11
AZ121703
LOCUS       AZ121703                 127 bp    DNA     linear   GSS 12-MAY-2000
DEFINITION  RPCI-23-479G20.TV RPCI-23 Mus musculus genomic clone
            RPCI-23-479G20, genomic survey sequence.
ACCESSION   AZ121703
VERSION     AZ121703.1  GI:7788873
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 127)
  AUTHORS   Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,
            Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de
            Jong,P. and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-23
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: RPCI-23-479G20.TJ
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-23. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
            or from Resea ch Genetics (info@resgen.com). BAC end page:
            http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 479  row: G  column: 20
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .127
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="RPCI-23-479G20"
                     /sex="Female"
                     /lab_host="DH10B"
                     /clone_lib="RPCI-23"
                     /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
                     EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
                     brain genomic DNA was isolated and  partially digested
                     with a combination of EcoRI and EcoRI Methylase.   Size
                     selected DNA was cloned into the pBACe3.6 vector at the
                     EcoRI  sites.  The ligation products were transformed into
                     DH10B  electrocompetent cells (BRL Life Technologies).   "
ORIGIN

  Query Match             51.8%;  Score 17.6;  DB 28;  Length 127;
  Best Local Similarity   53.1%;  Pred. No. 5.8e+03;
  Matches   17;  Conservative    6;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          2 UGGGGACUAUACCGCGUAAUGCUGCCUCCCCA 33
              :|||||| |: | | |:||:  : ||:| | |
Db          6 TGGGGACAATTCAGAGTAATAGTACCTCTCAA 37


RESULT 12
BB170705
LOCUS       BB170705                 168 bp    mRNA    linear   EST 29-JUN-2000
DEFINITION  BB170705 RIKEN full-length enriched, adult male hypothalamus Mus
            musculus cDNA clone A230020I19 3', mRNA sequence.
ACCESSION   BB170705
VERSION     BB170705.1  GI:8829788
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 168)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T.,
            Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C.,
            Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,
            Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K.,
            Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A.,
            Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A.,
            Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A.,
            Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
            Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length
            cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
            Okazaki,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .168
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="A230020I19"
                     /sex="male"
                     /tissue_type="hypothalamus"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="RIKEN full-length enriched, adult male
                     hypothalamus"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 20.0 and subtraction to Rot = 459.0. Second
                     strand cDNA was prepared with the primer adapter of
                     sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC
```

3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. "
ORIGIN

Query Match 51.8%; Score 17.6; DB 10; Length 168;
Best Local Similarity 50.0%; Pred. No. 6.3e+03;
Matches 16; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

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Qy          1 AUGGGGACUAUACCGCGUAAUGCUGCCUCCCC 32
              |:| ||||:|:  |  |: |: |: ||: |||
Db        118 ATGCGGACTATGACCTGTGATACTACCTTCCC 149
```

RESULT 13
CG613410
LOCUS CG613410 97 bp DNA linear GSS 02-OCT-2003
DEFINITION OST300555 Mus musculus 129Sv/Ev Mus musculus genomic clone OST300555, genomic survey sequence.
ACCESSION CG613410
VERSION CG613410.1 GI:37437259
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 97)
AUTHORS Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J., Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A., Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C., Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N., Zhu,Q., Person,C. and Sands,A.T.
TITLE Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT Contact: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
FEATURES Location/Qualifiers
source 1. .97
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129SV/EV"
/db_xref="taxon:10090"
/clone="OST300555"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"
ORIGIN

Query Match 51.2%; Score 17.4; DB 29; Length 97;
Best Local Similarity 57.1%; Pred. No. 6.5e+03;
Matches 16; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

```
Qy          3 GGGGACUAUACCGCGUAAUGCUGCCUCC 30
              | |||   :|||| |:  :|:|:|||:||
Db         36 GNGGATGCTACCGAGTCCTGCTGCCTCC 63
```

RESULT 14
CK296959
LOCUS CK296959 160 bp mRNA linear EST 15-DEC-2003
DEFINITION EST759673 Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length Nicotiana benthamiana cDNA clone NBMD548 3' end, mRNA sequence.
ACCESSION CK296959
VERSION CK296959.1 GI:39882864
KEYWORDS EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 160)
AUTHORS Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B., Staskawicz,B., Jin,H. and Baker,B.
TITLE Generation of EST sequences from Nicotiana benthamiana
JOURNAL Unpublished (2003)
COMMENT Other_ESTs: EST759672
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: GTA ATA CGA CTC ACT ATA GGG C.
FEATURES Location/Qualifiers
source 1. .160
/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NBMD548"
/tissue_type="abiotic and biotic stress-treated leaves, callus tissue and root tissue"
/lab_host="DH10B-TonA"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length"
/note="Vector: pCMVSport6.1; Site_1: EcoRI; Site_2: NotI; supplier: RNA was isolated from Nicotiana benthamiana tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Pseudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar amounts."
ORIGIN

Query Match 51.2%; Score 17.4; DB 14; Length 160;
Best Local Similarity 59.3%; Pred. No. 7.5e+03;
Matches 16; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

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Qy          8 CUAUACCGCGUAAUGCUGCCUCCCCAU 34
              |:  ||||  :||:||:||| |||| :
Db         50 CTTGACCGAATAATGCTGCCCCCCCCT 76
```

RESULT 15
AZ512563/c
LOCUS AZ512563 56 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0358G13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0358G13 F, genomic survey sequence.
ACCESSION AZ512563
VERSION AZ512563.1 GI:10693879
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 56)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0358 row: G column: 13
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 56.

FEATURES Location/Qualifiers
source 1. .56
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0358G13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 50.6%; Score 17.2; DB 28; Length 56;
Best Local Similarity 63.6%; Pred. No. 6.7e+03;
Matches 14; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

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Qy         13 CCGCGUAAUGCUGCCUCCCCAU 34
              | | |:||: |:|||:|||||:
Db         24 CAGAGTAATCCTGCCTCCCCAT 3
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Search completed: April 9, 2004, 06:03:59
Job time : 1044.9 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 9, 2004, 01:42:24 ; Search time 241.439 Seconds
(without alignments)
5206.064 Million cell updates/sec

Title: US-09-963-827B-71
Perfect score: 29
Sequence: 1 ggggacuauaccggcaaucgugcaucccc 29

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 2199298

Minimum DB seq length: 0
Maximum DB seq length: 200

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
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22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	19	65.5	169	6	AR051528	AR051528 Sequence
c	2	19	65.5	169	6	AR072668	AR072668 Sequence
c	3	19	65.5	169	6	AR073213	AR073213 Sequence
	4	17.8	61.4	101	11	G43342	G43342 WIAF-2007-S
	5	16.8	57.9	166	6	AX923424	AX923424 Sequence
	6	16.8	57.9	181	6	AX923425	AX923425 Sequence
	7	16.4	56.6	160	11	AB059077	AB059077 Sus scrof
c	8	16	55.2	51	5	ECY17989	Y17989 Enchelyopus
c	9	15.8	54.5	105	6	AX694803	AX694803 Sequence
	10	15.6	53.8	60	1	AF178261S1	AF178261 Chlamydia
	11	15.6	53.8	60	1	AF178265S1	AF178265 Chlamydia
	12	15.6	53.8	60	1	AF178269S1	AF178269 Chlamydia
	13	15.6	53.8	60	1	AF178273S1	AF178273 Chlamydia
	14	15.4	53.1	79	5	S67413	S67413 Xenopus lae
c	15	15.4	53.1	108	6	AX683332	AX683332 Sequence
	16	15.2	52.4	71	6	AR058826	AR058826 Sequence
	17	15.2	52.4	71	6	AR063552	AR063552 Sequence
	18	15.2	52.4	71	6	AR140942	AR140942 Sequence
	19	15.2	52.4	151	6	AX867991	AX867991 Sequence
	20	15.2	52.4	151	6	BD148053	BD148053 Primer fo
c	21	15.2	52.4	174	9	F320227S16	AF320242 Homo sapi
	22	15	51.7	132	9	F320227S10	AF320236 Homo sapi
c	23	15	51.7	155	6	AR051547	AR051547 Sequence
c	24	15	51.7	155	6	AR072687	AR072687 Sequence
c	25	15	51.7	155	6	AR073232	AR073232 Sequence
	26	14.8	51.0	47	6	AR171238	AR171238 Sequence
	27	14.8	51.0	64	17	HSMC24G11	X88248 H.sapiens D
c	28	14.8	51.0	68	9	HUMTCVD1AI	L32381 Human (clon
c	29	14.6	50.3	50	6	AX164814	AX164814 Sequence
	30	14.6	50.3	94	9	AF150996	AF150996 Homo sapi
c	31	14.6	50.3	105	6	BD261167	BD261167 Methods f
c	32	14.6	50.3	105	6	BD273668	BD273668 Protein t
c	33	14.6	50.3	105	6	BD139195	BD139195 Anti-path
	34	14.6	50.3	138	5	AB042992	AB042992 Chrysophr
	35	14.6	50.3	157	6	AX902921	AX902921 Sequence
	36	14.6	50.3	157	6	BD038454	BD038454 Sequence
c	37	14.6	50.3	172	11	DM118G9T	Z50272 D. melanoga
	38	14.6	50.3	187	9	HSU15687	U15687 Human clone
	39	14.6	50.3	189	9	HSU15686	U15686 Human clone
	40	14.6	50.3	198	1	AF064198	AF064198 Streptomy
	41	14.6	50.3	198	1	AF064199	AF064199 Streptomy
c	42	14.4	49.7	31	6	AX248328	AX248328 Sequence
c	43	14.4	49.7	36	6	AR336716	AR336716 Sequence
c	44	14.4	49.7	41	6	AR176221	AR176221 Sequence
c	45	14.4	49.7	41	6	AX003193	AX003193 Sequence

ALIGNMENTS

RESULT 1
AR051528/c
LOCUS AR051528 169 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 98 from patent US 5830670.
ACCESSION AR051528
VERSION AR051528.1 GI:5974892
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 169)
AUTHORS de la Monte,S. and Wands,J.R.
TITLE Neural thread protein gene expression and detection of Alzheimer's disease
JOURNAL Patent: US 5830670-A 98 03-NOV-1998;

```
FEATURES             Location/Qualifiers
     source          1. .169
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             65.5%;  Score 19;  DB 6;  Length 169;
  Best Local Similarity   70.4%;  Pred. No. 6.1e+02;
  Matches   19;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 GGACUAUACCGGCAAUCGUGCAUCCCC 29
              |||| | | |||| |:||:|| :||||
Db         36 GGACCAAAGCGGCCATCGTGCCTCCCC 10


RESULT 2
AR072668/c
LOCUS       AR072668                169 bp    DNA     linear   PAT 28-AUG-2000
DEFINITION  Sequence 98 from patent US 5948634.
ACCESSION   AR072668
VERSION     AR072668.1  GI:9999432
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 169)
  AUTHORS   de la Monte,S. and Wands,J.R.
  TITLE     Neural thread protein gene expression and detection of alzheimer's
            disease
  JOURNAL   Patent: US 5948634-A 98 07-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .169
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             65.5%;  Score 19;  DB 6;  Length 169;
  Best Local Similarity   70.4%;  Pred. No. 6.1e+02;
  Matches   19;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 GGACUAUACCGGCAAUCGUGCAUCCCC 29
              |||| | | |||| |:||:|| :||||
Db         36 GGACCAAAGCGGCCATCGTGCCTCCCC 10


RESULT 3
AR073213/c
LOCUS       AR073213                169 bp    DNA     linear   PAT 28-AUG-2000
DEFINITION  Sequence 98 from patent US 5948888.
ACCESSION   AR073213
VERSION     AR073213.1  GI:9999976
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 169)
  AUTHORS   de la Monte,S. and Wands,J.R.
  TITLE     Neural thread protein gene expression and detection of Alzheimer's
            disease
  JOURNAL   Patent: US 5948888-A 98 07-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .169
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             65.5%;  Score 19;  DB 6;  Length 169;
  Best Local Similarity   70.4%;  Pred. No. 6.1e+02;
  Matches   19;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 GGACUAUACCGGCAAUCGUGCAUCCCC 29
              |||| | | |||| |:||:|| :||||
Db         36 GGACCAAAGCGGCCATCGTGCCTCCCC 10


RESULT 4
G43342
LOCUS       G43342                  101 bp    mRNA    linear   STS 27-JAN-1999
DEFINITION  WIAF-2007-STS Human THudson EST Homo sapiens STS cDNA, sequence
            tagged site.
ACCESSION   G43342
VERSION     G43342.1  GI:4192259
KEYWORDS    STS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 101)
  AUTHORS   Wang,D.G., Fan,J.B., Siao,C.J., Berno,A., Young,P., Sapolsky,R.,
            Ghandour,G., Perkins,N., Winchester,E., Spencer,J., Kruglyak,L.,
            Stein,L., Hsie,L., Topaloglou,T., Hubbell,E., Robinson,E.,
            Mittmann,M., Morris,M.S., Shen,N., Kilburn,D., Rioux,J.,
            Nusbaum,C., Rozen,S., Hudson,T.J., Lipshutz,R., Chee,M. and
            Lander,E.S.
  TITLE     Large-scale identification, mapping, and genotyping of
            single-nucleotide polymorphisms in the human genome
  JOURNAL   Science 280 (5366), 1077-1082 (1998)
  MEDLINE   98248615
   PUBMED   9582121
COMMENT     Synonyms: CL_EST232115
            Contact: Thomas Hudson
            Whitehead Institute/MIT Center for Genome Research
            Whitehead Institute for Biomedical Research
            9 Cambridge Center, Cambridge MA 02142 USA
            Tel: 617 252 1900
            Fax: 617 252 1902
            Email: thudson@genome.wi.mit.edu
            Primer A: TAAAACATACGAGTACTGTACACGC
            Primer B: TCCCCTCCTGAATATACAACG
            STS size: 101
            PCR Profile:
                    Presoak:            94 degrees C for 4.00 minutes
                    Denaturation:       94 degrees C for 50.0 seconds
                    Annealing:          58 degrees C for 1.50 minutes
                    Polymerization:     72 degrees C for 1.00 minutes
                    PCR Cycles:         30
                    Thermal Cycler: custom built by IAS, Costar, Cambridge MA
            Protocol:
                  Template:       10 ng
                  Primer:         each 5 pM
                  dNTPs:          4 nM
                  Taq Polymerase: 0.5 U
                  Total Vol:      20 uL

            Buffer:
                  Mg2+:          1.5 mM
                  KCl:            50 mM
                  Tris-HCl:       10 mM
                  Gelatin:      .001 %.
FEATURES             Location/Qualifiers
     source          1. .101
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /map="147.90 cR from top of Chr1 linkage group"
                     /clone_lib="Human THudson EST"
                     /note="STSs derived from sequences in dbEST and the
                     Unigene collection."
     STS             1. .101
     primer_bind     1. .25
     primer_bind     complement(81. .101)
ORIGIN

  Query Match             61.4%;  Score 17.8;  DB 11;  Length 101;
  Best Local Similarity   62.1%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    4;  Mismatches    7;  Indels    0;  Gaps    0;
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Qy          1 GGGGACUAUACCGGCAAUCGUGCAUCCCC 29
              | | ||: :||  |||| | :|||:||||
Db         11 GAGTACTGTACACGCAAGCATGCATCCCC 39


RESULT 5
AX923424
LOCUS       AX923424                166 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1 from Patent WO03080816.
ACCESSION   AX923424
VERSION     AX923424.1  GI:40216473
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Andrews,P. and Draper,J.
  TITLE     Stem cell culture
  JOURNAL   Patent: WO 03080816-A 1 02-OCT-2003;
            THE UNIVERSITY OF SHEFFIELD (GB)
FEATURES             Location/Qualifiers
     source          1. .166
                     /organism="Mus musculus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10090"
ORIGIN

  Query Match             57.9%;  Score 16.8;  DB 6;  Length 166;
  Best Local Similarity   60.7%;  Pred. No. 6.9e+03;
  Matches   17;  Conservative    4;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 GGGGACUAUACCGGCAAUCGUGCAUCCC 28
              ||||||:|: ||| ||    :|| :|||
Db         67 GGGGACTATCCCGCCACCGTTGCGTCCC 94


RESULT 6
AX923425
LOCUS       AX923425                181 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 2 from Patent WO03080816.
ACCESSION   AX923425
VERSION     AX923425.1  GI:40216474
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Andrews,P. and Draper,J.
  TITLE     Stem cell culture
  JOURNAL   Patent: WO 03080816-A 2 02-OCT-2003;
            THE UNIVERSITY OF SHEFFIELD (GB)
FEATURES             Location/Qualifiers
     source          1. .181
                     /organism="Mus musculus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10090"
ORIGIN

  Query Match             57.9%;  Score 16.8;  DB 6;  Length 181;
  Best Local Similarity   60.7%;  Pred. No. 6.9e+03;
  Matches   17;  Conservative    4;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 GGGGACUAUACCGGCAAUCGUGCAUCCC 28
              ||||||:|: ||| ||    :|| :|||
Db         67 GGGGACTATCCCGCCACCGTTGCGTCCC 94


RESULT 7
AB059077
LOCUS       AB059077                160 bp    DNA     linear   STS 19-MAR-2002
DEFINITION  Sus scrofa domestica genomic DNA, chromosome 10, 346B10F, sequence
            tagged site.
ACCESSION   AB059077
VERSION     AB059077.1  GI:19570610
KEYWORDS    STS.
SOURCE      Sus scrofa domestica (domestic pig)
  ORGANISM  Sus scrofa domestica
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1
  AUTHORS   Kiuchi,S., Inage,Y., Hiraiwa,H., Uenishi,H. and Yasue,H.
  TITLE     Assignment of 280 swine genomic inserts including 31
            microsatellites from BAC clones to the swine RH map (IMpRH map)
  JOURNAL   Mamm. Genome 13 (2), 80-88 (2002)
  MEDLINE   21886643
   PUBMED   11889555
REFERENCE   2  (bases 1 to 160)
  AUTHORS   Kiuchi,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-MAR-2001) Sachiko Kiuchi, National Institute of
            Agrobiological Sciences, Genome Research Group; 2 Ikenodai,
            Kukizaki-machi, Inashiki-gun, Ibaraki 305-0901, Japan
            (E-mail:sachikok@affrc.go.jp, Tel:81-298-38-8664,
            Fax:81-298-38-8674)
FEATURES             Location/Qualifiers
     source          1. .160
                     /organism="Sus scrofa domestica"
                     /mol_type="genomic DNA"
                     /sub_species="domestica"
                     /db_xref="taxon:9825"
                     /chromosome="10"
                     /clone="346B10"
                     /clone_lib="Swine genomic BAC library, National Institute
                     of Agrobiological Resources, Ibaraki, Japan"
                     /note="synonym:Sus scrofa domesticus"
     STS             1. .160
                     /standard_name="346B10F"
     primer_bind     1. .20
                     /PCR_conditions="denaturation 30s at 95 degrees, annealing
                     30s at 57 degrees, extension 30s at 72 degrees, final
                     elongation 5min at 72 degrees, 35 cycles"
     primer_bind     complement(141. .160)
ORIGIN

  Query Match             56.6%;  Score 16.4;  DB 11;  Length 160;
  Best Local Similarity   61.5%;  Pred. No. 1.1e+04;
  Matches   16;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          4 GACUAUACCGGCAAUCGUGCAUCCCC 29
              |||:| | | ||||: |:|| : |||
Db        128 GACTACAACAGCAATTGTGCTTACCC 153


RESULT 8
ECY17989/c
LOCUS       ECY17989                51 bp    DNA     linear   VRT 29-MAR-2000
DEFINITION  Enchelyopus cimbrius mitochondrial intergenic spacer and partial
            tRNA-Thr and tRNA-Pro genes.
ACCESSION   Y17989
VERSION     Y17989.1  GI:3717962
KEYWORDS    intergenic spacer; transfer RNA-Pro; tRNA-Pro gene.
SOURCE      mitochondrion Enchelyopus cimbrius (fourbeard rockling)
  ORGANISM  Enchelyopus cimbrius
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Paracanthopterygii; Gadiformes; Gaidropsaridae;
            Enchelyopus.
REFERENCE   1
  AUTHORS   Bakke I,I., Shields,G.F. and Johansen,S.
  TITLE     Sequence Characterization of a Unique Intergenic Spacer in
            Gadiformes Mitochondrial DNA
  JOURNAL   Mar. Biotechnol. 1 (5), 411-0415 (1999)
   PUBMED   10525675
```

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REFERENCE   2  (bases 1 to 51)
  AUTHORS   Johansen,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-AUG-1998) S. Johansen, Institution University of
            Tromso, Department of Molecular Cell Biology, IMB, University of
            Tromso, 9037 Tromso, NORWAY
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Enchelyopus cimbrius"
                     /organelle="mitochondrion"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:81640"
     gene            1. .13
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     tRNA            <1. .13
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                     /product="tRNA-Thr"
     misc_feature    14. .39
                     /note="intergenic spacer"
     gene            40. .51
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                     /gene="tRNA-Pro"
                     /product="tRNA-Pro"
ORIGIN

  Query Match             55.2%;  Score 16;  DB 5;  Length 51;
  Best Local Similarity   70.8%;  Pred. No. 1.7e+04;
  Matches   17;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GGGGACUAUACCGGCAAUCGUGCA 24
              |||| |:| ||||| ||  |:|||
Db         33 GGGGCCTAAACCGGTAAATGTGCA 10


RESULT 9
AX694803/c
LOCUS       AX694803                105 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 430 from Patent WO03008583.
ACCESSION   AX694803
VERSION     AX694803.1  GI:29417915
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Morris,D.W. and Engelhard,E.K.
  TITLE     Novel compositions and methods for cancer
  JOURNAL   Patent: WO 03008583-A 430 30-JAN-2003;
            Sagres Discovery (US)
FEATURES             Location/Qualifiers
     source          1. .105
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                     /db_xref="taxon:10090"
ORIGIN

  Query Match             54.5%;  Score 15.8;  DB 6;  Length 105;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+04;
  Matches   14;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 GGGACUAUACCGGCAAUCG 20
              || ||:|:|| |||||:||
Db         27 GGTACTATACTGGCAATCG 9


RESULT 10
AF178261S1
LOCUS       AF178261S1              60 bp    DNA     linear   BCT 20-JAN-2000
DEFINITION  Chlamydia trachomatis isolate CA46 major outer membrane protein
            (omp1) gene, variable domain 1.
ACCESSION   AF178261
VERSION     AF178261.1  GI:6716617
KEYWORDS    .
SEGMENT     1 of 4
SOURCE      Chlamydia trachomatis
  ORGANISM  Chlamydia trachomatis
            Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
REFERENCE   1  (bases 1 to 60)
  AUTHORS   Sturm-Ramirez,K., Brumblay,H., Diop,K., Gueye-Ndiaye,A.,
            Sankale,J.L., Thior,I., N'Doye,I., Hsieh,C.C., Mboup,S. and
            Kanki,P.J.
  TITLE     Molecular epidemiology of genital Chlamydia trachomatis infection
            in high-risk women in Senegal, West Africa
  JOURNAL   J. Clin. Microbiol. 38 (1), 138-145 (2000)
  MEDLINE   20085123
   PUBMED   10618077
REFERENCE   2  (bases 1 to 60)
  AUTHORS   Sturm-Ramirez,K., Brumblay,H., Diop,K., Gueye-Ndiaye,A.,
            Sankale,J.L., Thior,I., N'Doye,I., Hsieh,C.C., Mboup,S. and
            Kanki,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-AUG-1999) Immunology and Infectious Diseases, Harvard
            School of Public Health, 651 Huntington Ave., Boston, MA 02115, USA
FEATURES .           Location/Qualifiers
     source          1. .60
                     /organism="Chlamydia trachomatis"
                     /mol_type="genomic DNA"
                     /isolate="CA46"
                     /db_xref="taxon:813"
                     /country="Senegal"
     misc_feature    1. .60
                     /gene="omp1"
                     /note="variable domain 1"
ORIGIN

  Query Match             53.8%;  Score 15.6;  DB 1;  Length 60;
  Best Local Similarity   68.2%;  Pred. No. 2.7e+04;
  Matches   15;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          8 AUACCGGCAAUCGUGCAUCCCC 29
              |:|| |||||: |:||| | ||
Db         17 ATACAGGCAATAGTGCAGCTCC 38


RESULT 11
AF178265S1
LOCUS       AF178265S1              60 bp    DNA     linear   BCT 20-JAN-2000
DEFINITION  Chlamydia trachomatis isolate CA599 major outer membrane protein
            (omp1) gene, variable domain 1.
ACCESSION   AF178265
VERSION     AF178265.1  GI:6716621
KEYWORDS    .
SEGMENT     1 of 4
SOURCE      Chlamydia trachomatis
  ORGANISM  Chlamydia trachomatis
            Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
REFERENCE   1  (bases 1 to 60)
  AUTHORS   Sturm-Ramirez,K., Brumblay,H., Diop,K., Gueye-Ndiaye,A.,
            Sankale,J.L., Thior,I., N'Doye,I., Hsieh,C.C., Mboup,S. and
            Kanki,P.J.
  TITLE     Molecular epidemiology of genital Chlamydia trachomatis infection
            in high-risk women in Senegal, West Africa
  JOURNAL   J. Clin. Microbiol. 38 (1), 138-145 (2000)
  MEDLINE   20085123
   PUBMED   10618077
REFERENCE   2  (bases 1 to 60)
  AUTHORS   Sturm-Ramirez,K., Brumblay,H., Diop,K., Gueye-Ndiaye,A.,
            Sankale,J.L., Thior,I., N'Doye,I., Hsieh,C.C., Mboup,S. and
            Kanki,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-AUG-1999) Immunology and Infectious Diseases, Harvard
            School of Public Health, 651 Huntington Ave., Boston, MA 02115, USA
FEATURES             Location/Qualifiers
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                     /organism="Chlamydia trachomatis"
                     /mol_type="genomic DNA"
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                     /note="variable domain 1"
ORIGIN

  Query Match             53.8%;  Score 15.6;  DB 1;  Length 60;
  Best Local Similarity   68.2%;  Pred. No. 2.7e+04;
  Matches   15;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          8 AUACCGGCAAUCGUGCAUCCCC 29
              |:|| ||||| |:||| | ||
Db         17 ATACAGGCAATAGTGCAGCTCC 38


RESULT 12
AF178269S1
LOCUS       AF178269S1               60 bp    DNA     linear   BCT 20-JAN-2000
DEFINITION  Chlamydia trachomatis isolate CA543 major outer membrane protein
            (omp1) gene, variable domain 1.
ACCESSION   AF178269
VERSION     AF178269.1  GI:6716625
KEYWORDS    .
SEGMENT     1 of 4
SOURCE      Chlamydia trachomatis
  ORGANISM  Chlamydia trachomatis
            Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
REFERENCE   1  (bases 1 to 60)
  AUTHORS   Sturm-Ramirez,K., Brumblay,H., Diop,K., Gueye-Ndiaye,A.,
    .       Sankale,J.L., Thior,I., N'Doye,I., Hsieh,C.C., Mboup,S. and
            Kanki,P.J.
  TITLE     Molecular epidemiology of genital Chlamydia trachomatis infection
            in high-risk women in Senegal, West Africa
  JOURNAL   J. Clin. Microbiol. 38 (1), 138-145 (2000)
  MEDLINE   20085123
   PUBMED   10618077
REFERENCE   2  (bases 1 to 60)
  AUTHORS   Sturm-Ramirez,K., Brumblay,H., Diop,K., Gueye-Ndiaye,A.,
            Sankale,J.L., Thior,I., N'Doye,I., Hsieh,C.C., Mboup,S. and
            Kanki,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-AUG-1999) Immunology and Infectious Diseases, Harvard
            School of Public Health, 651 Huntington Ave., Boston, MA 02115, USA
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /isolate="CA543"
                     /db_xref="taxon:813"
                     /country="Senegal"
     misc_feature    1. .60
                     /gene="omp1"
                     /note="variable domain 1"
ORIGIN

  Query Match             53.8%;  Score 15.6;  DB 1;  Length 60;
  Best Local Similarity   68.2%;  Pred. No. 2.7e+04;
  Matches   15;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          8 AUACCGGCAAUCGUGCAUCCCC 29
              |:|| ||||| |:||| | ||
Db         17 ATACAGGCAATAGTGCAGCTCC 38


RESULT 13
AF178273S1
LOCUS       AF178273S1               60 bp    DNA     linear   BCT 20-JAN-2000
DEFINITION  Chlamydia trachomatis isolate CA584 major outer membrane protein
            (omp1) gene, variable domain 1.
ACCESSION   AF178273
VERSION     AF178273.1  GI:6716629
KEYWORDS    .
SEGMENT     1 of 4
SOURCE      Chlamydia trachomatis
  ORGANISM  Chlamydia trachomatis
            Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
REFERENCE   1  (bases 1 to 60)
  AUTHORS   Sturm-Ramirez,K., Brumblay,H., Diop,K., Gueye-Ndiaye,A.,
            Sankale,J.L., Thior,I., N'Doye,I., Hsieh,C.C., Mboup,S. and
            Kanki,P.J.
  TITLE     Molecular epidemiology of genital Chlamydia trachomatis infection
            in high-risk women in Senegal, West Africa
  JOURNAL   J. Clin. Microbiol. 38 (1), 138-145 (2000)
  MEDLINE   20085123
   PUBMED   10618077
REFERENCE   2  (bases 1 to 60)
  AUTHORS   Sturm-Ramirez,K., Brumblay,H., Diop,K., Gueye-Ndiaye,A.,
            Sankale,J.L., Thior,I., N'Doye,I., Hsieh,C.C., Mboup,S. and
            Kanki,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-AUG-1999) Immunology and Infectious Diseases, Harvard
            School of Public Health, 651 Huntington Ave., Boston, MA 02115, USA
FEATURES             Location/Qualifiers
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                     /organism="Chlamydia trachomatis"
                     /mol_type="genomic DNA"
                     /isolate="CA584"
                     /db_xref="taxon:813"
                     /country="Senegal"
     misc_feature    1. .60
                     /gene="omp1"
                     /note="variable domain 1"
ORIGIN

  Query Match             53.8%;  Score 15.6;  DB 1;  Length 60;
  Best Local Similarity   68.2%;  Pred. No. 2.7e+04;
  Matches   15;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          8 AUACCGGCAAUCGUGCAUCCCC 29
              |:|| ||||| |:||| | ||
Db         17 ATACAGGCAATAGTGCAGCTCC 38


RESULT 14
S67413
LOCUS       S67413                   79 bp    RNA     linear   VRT 10-MAY-2002
DEFINITION  Xenopus laevis short interspersed repeat Xlsirtp11-1 sequence.
ACCESSION   S67413
VERSION     S67413.1  GI:456935
KEYWORDS    .
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus.
REFERENCE   1  (bases 1 to 79)
  AUTHORS   Kloc,M., Spohr,G. and Etkin,L.D.
  TITLE     Translocation of repetitive RNA sequences with the germ plasm in
            Xenopus oocytes
  JOURNAL   Science 262 (5140), 1712-1714 (1993)
  MEDLINE   94082288
   PUBMED   7505061
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 141085] from the original journal article.
            This sequence comes from Fig. 1.
FEATURES             Location/Qualifiers
     source          1. .79
                     /organism="Xenopus laevis"
                     /mol_type="genomic RNA"
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                     /cell_type="oocyte"
     repeat_region   1. .79
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                     /note="short interspersed repeat Xlsirtp11-1"
ORIGIN

  Query Match             53.1%;  Score 15.4;  DB 5;  Length 79;
  Best Local Similarity   64.0%;  Pred. No. 3.3e+04;
  Matches   16;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          5 ACUAUACCGGCAAUCGUGCAUCCCC 29
              ||:|:||| || |:|   || ||||
Db         24 ACTATACCTGCTATCCCACAGCCCC 48


RESULT 15
AX683332/c
LOCUS       AX683332                 108 bp    DNA     linear   PAT 29-MAR-2003
DEFINITION  Sequence 48 from Patent WO03008578.
ACCESSION   AX683332
VERSION     AX683332.1  GI:29370485
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Primiano,T., Chang,B.D. and Roninson,I.B.
  TITLE     Reagents and methods for identifying gene targets for treating
            cancer
  JOURNAL   Patent: WO 03008578-A 48 30-JAN-2003;
            THE BOARD OF TRUSTEES OF THE UNIVERSITY OF ILLINOIS (US)
FEATURES             Location/Qualifiers
     source          1. .108
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             53.1%;  Score 15.4;  DB 6;  Length 108;
  Best Local Similarity   60.0%;  Pred. No. 3.3e+04;
  Matches   15;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          5 ACUAUACCGGCAAUCGUGCAUCCCC 29
              ||:  || |||| :||:|||:  ||
Db         78 ACTTCACGGGCAGTCGTGCATTTCC 54


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Job time : 244.439 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 9, 2004, 01:39:24 ; Search time 103.035 Seconds
(without alignments)
1195.685 Million cell updates/sec

Title: US-09-963-827B-71
Perfect score: 29
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 3774412

Minimum DB seq length: 0
Maximum DB seq length: 200

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	29	100.0	29	6	ABN88558	Abn88558 Coagulati
	2	29	100.0	29	7	ABZ21243	Abz21243 FIXa apta
	3	29	100.0	33	7	ABZ21258	Abz21258 Aptamer 9
	4	29	100.0	96	6	ABN88504	Abn88504 Coagulati
c	5	19	65.5	169	2	AAT27772	Aat27772 Human neu
	6	17.8	61.4	96	6	ABN88494	Abn88494 Coagulati
	7	17.8	61.4	101	2	AAX11804	Aax11804 Human bia
	8	16.8	57.9	166	9	ADE35061	Ade35061 Mouse fib
	9	16.8	57.9	181	9	ADE35062	Ade35062 Mouse fib
	10	16.2	55.9	29	7	ABZ21255	Abz21255 FIXa apta
	11	16.2	55.9	95	6	ABN88499	Abn88499 Coagulati
	12	16	55.2	172	7	ABX91389	Abx91389 Murine ge
c	13	15.8	54.5	50	6	ABZ01528	Abz01528 Human leu
c	14	15.8	54.5	105	8	ADA01911	Ada01911 Mouse car
c	15	15.8	54.5	105	9	ADB71650	Adb71650 Mouse car
	16	15.6	53.8	60	1	AAN97053	Aan97053 Sequence
	17	15.6	53.8	60	1	AAN92135	Aan92135 Sequence
	18	15.6	53.8	60	2	AAX18012	Aax18012 C. tracho
	19	15.6	53.8	60	6	ABK97729	Abk97729 C. tracho
	20	15.6	53.8	60	6	ABK97792	Abk97792 Chlamydia
c	21	15.4	53.1	108	7	ACF19007	Acf19007 Tumour ce
c	22	15.4	53.1	108	9	ADC84830	Adc84830 MCF-7 bre
	23	15.2	52.4	71	2	AAT65332	Aat65332 Human ker
	24	15.2	52.4	96	6	ABN88501	Abn88501 Coagulati
	25	15.2	52.4	100	7	ACD76502	Acd76502 E. coli K
	26	15.2	52.4	151	4	AAH06061	Aah06061 Human cDN
c	27	15.2	52.4	184	9	ADD49611	Add49611 Human lun
c	28	14.8	51.0	31	4	AAI29919	Aai29919 Human sin
	29	14.8	51.0	47	2	AAZ09656	Aaz09656 Human uri
	30	14.8	51.0	47	6	AAD21962	Aad21962 Human uro
	31	14.8	51.0	47	9	ADC72162	Adc72162 Human uro
	32	14.8	51.0	100	7	ACD77813	Acd77813 E. coli K
c	33	14.8	51.0	177	9	ADD25152	Add25152 Fertility
c	34	14.6	50.3	40	9	ADC42545	Adc42545 FANCD2 PC
c	35	14.6	50.3	50	5	ABL00018	Abl00018 Human sil
c	36	14.6	50.3	100	7	ACD73338	Acd73338 E. coli K
c	37	14.6	50.3	100	7	ACD73340	Acd73340 E. coli K
c	38	14.6	50.3	100	7	ACD73339	Acd73339 E. coli K
c	39	14.6	50.3	100	7	ACD77784	Acd77784 E. coli K
	40	14.6	50.3	100	7	ACD70809	Acd70809 E. coli K
c	41	14.6	50.3	105	3	AAC63858	Aac63858 pTAT link
	42	14.6	50.3	157	3	AAC14709	Aac14709 Human sec
	43	14.6	50.3	196	5	ABV56743	Abv56743 Human pro
	44	14.6	50.3	198	4	AAK46529	Aak46529 Human bon
	45	14.6	50.3	198	4	ABS46296	Abs46296 Human liv

ALIGNMENTS

RESULT 1
ABN88558
ID ABN88558 standard; RNA; 29 BP.
XX
AC ABN88558;
XX
DT 19-AUG-2002 (first entry)
XX
DE Coagulation factor IXa (FIXa) aptamer SEQ ID NO:71.
XX
KW RNA aptamer; identification; coagulation factor; angiopoietin; thrombin;
KW E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant;
KW cell proliferation; intimal hyperplasia; angiogenesis;
KW bypass graft surgery; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200226932-A2.
XX
PD 04-APR-2002.
XX
PF 26-SEP-2001; 2001WO-US030004.
XX
PR 26-SEP-2000; 2000US-0235654P.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Sullenger BA, Rusconi CP;
XX
DR WPI; 2002-479560/51.
XX
PT Novel RNA aptamers that selectively bind coagulation pathway factors, E2F
PT family members, Ang1 or Ang2, useful for modulating coagulation pathway
PT factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.
XX
PS Claim 14; Page 25; 216pp; English.
XX
CC The present invention describes RNA aptamers (I,II,III) that selectively
CC bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c)
CC angiopoietin-1 (Ang1) or Ang2, respectively, where (I), (II), (III) have
CC a dissociation constant for the coagulation pathway factor, an E2F family
CC member, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) have
CC cardiant and cytostatic activities. (I) are useful for modulating the
CC biological activity of a coagulation pathway factor which involves
CC administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that

```
CC   the biological activity of the coagulation pathway factor in the warm-
CC   blooded vertebrate is modulated. (I) are also useful for treating
CC   cardiovascular diseases in the mammal. (II) are useful for modulating E2F
CC   activity in a warm-blooded vertebrate. (III) are useful for modulating
CC   Ang1 or Ang2 activity in a warm-blooded vertebrate. (I) are potent
CC   anticoagulants and significantly delay the clotting time of normal human
CC   plasma or the activation of platelets in response to thrombin. (II) are
CC   useful for inhibiting cell proliferation in a number of conditions e.g.,
CC   intimal hyperplasia following bypass graft surgery. (III) are useful for
CC   modulating angiogenesis. The RNA aptamers are also useful for diagnostic,
CC   research and therapeutic context. The aptamers are useful as diagnostic
CC   reagents to detect the presence or absence of target substances to which
CC   they specifically bind, and for identifying substances to which they
CC   specifically bind, for isolating and purifying substances to which they
CC   bind, and as a separation reagent for retrieving the targets to which
CC   they specifically bind. ABN88488 to ABN88713 and ABB81231 represent
CC   sequences used in the exemplification of the present invention
XX
SQ   Sequence 29 BP; 6 A; 10 C; 8 G; 0 T; 5 U; 0 Other;

  Query Match             100.0%;  Score 29;  DB 6;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 0.00031;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGGGACUAUACCGGCAAUCGUGCAUCCCC 29
              |||||||||||||||||||||||||||||
Db          1 GGGGACUAUACCGGCAAUCGUGCAUCCCC 29


RESULT 2
ABZ21243
ID   ABZ21243 standard; RNA; 29 BP.
XX
AC   ABZ21243;
XX
DT   16-APR-2003  (first entry)
XX
DE   FIXa aptamer, SEQ ID 3.
XX
KW   Immunosuppressive; aptamer; infection; autoimmunity; tumour;
KW   inflammatory proliferative disease; hypoglycaemia; human;
KW   coagulation Factor IXa; FIXa; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1. .5
FT                   /*tag=  a
FT                   /bound_moiety= "Nucleotides 25. .29"
FT   stem_loop       14. .23
FT                   /*tag=  b
FT   misc_binding    25. .29
FT                   /*tag=  c
FT                   /bound_moiety= "Nucleotides 1. .5"
XX
PN   WO200296926-A1.
XX
PD   05-DEC-2002.
XX
PF   28-MAY-2002; 2002WO-US016555.
XX
PR   25-MAY-2001; 2001US-0293231P.
PR   07-NOV-2001; 2001US-0331037P.
XX
PA   (UYDU-) UNIV DUKE.
XX
PI   Sullenger BA,  Rusconi C;
XX
DR   WPI; 2003-140438/13.
XX
PT   Altering affinity of nucleic acid ligands for target molecules in a
PT   patient or reversing binding of labeled ligands to target tissues, by
PT   administering (to a patient receiving the ligand) a modulator that binds
PT   to ligand.
XX
PS   Example 2; Fig 7; 111pp; English.
XX
CC   The present invention relates to a method for altering the affinity of a
CC   nucleic acid ligand (e.g. an aptamer) for a target molecule in a patient
CC   or in vitro, or reversing the binding of the labelled ligand to a target
CC   tissue. The method comprises administering a modulator that binds to the
CC   ligand to a patient receiving the ligand, or contacting the ligand with
CC   the modulator under conditions such that the modulator binds to the
CC   ligand, and thus alters the affinity of the ligand for the target
CC   molecule. The method is useful for treating a number of disorders e.g.
CC   infection, autoimmunity, tumours, inflammatory proliferative diseases and
CC   hypoglycaemia. The present sequence is an aptamer to human coagulation
CC   Factor IXa (FIXa aptamer), which was used to illustrate the method of the
CC   invention
XX
SQ   Sequence 29 BP; 6 A; 10 C; 8 G; 0 T; 5 U; 0 Other;

  Query Match             100.0%;  Score 29;  DB 7;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 0.00031;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGGGACUAUACCGGCAAUCGUGCAUCCCC 29
              |||||||||||||||||||||||||||||
Db          1 GGGGACUAUACCGGCAAUCGUGCAUCCCC 29


RESULT 3
ABZ21258
ID   ABZ21258 standard; RNA; 33 BP.
XX
AC   ABZ21258;
XX
DT   16-APR-2003  (first entry)
XX
DE   Aptamer 9.20t, SEQ ID 18.
XX
KW   Immunosuppressive; aptamer; infection; autoimmunity; tumour;
KW   inflammatory proliferative disease; hypoglycaemia; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1. .7
FT                   /*tag=  a
FT                   /bound_moiety= "Nucleotides 27. .33"
FT   stem_loop       16. .25
FT                   /*tag=  b
FT   misc_binding    27. .33
FT                   /*tag=  c
FT                   /bound_moiety= "Nucleotides 1. .7"
XX
PN   WO200296926-A1.
XX
PD   05-DEC-2002.
XX
PF   28-MAY-2002; 2002WO-US016555.
XX
PR   25-MAY-2001; 2001US-0293231P.
PR   07-NOV-2001; 2001US-0331037P.
XX
PA   (UYDU-) UNIV DUKE.
XX
PI   Sullenger BA,  Rusconi C;
XX
DR   WPI; 2003-140438/13.
XX
PT   Altering affinity of nucleic acid ligands for target molecules in a
PT   patient or reversing binding of labeled ligands to target tissues, by
PT   administering (to a patient receiving the ligand) a modulator that binds
PT   to ligand.
XX
```

PS Example 3; Fig 10A; 111pp; English.
XX
CC The present invention relates to a method for altering the affinity of a
CC nucleic acid ligand (e.g. an aptamer) for a target molecule in a patient
CC or in vitro, or reversing the binding of the labelled ligand to a target
CC tissue. The method comprises administering a modulator that binds to the
CC ligand to a patient receiving the ligand, or contacting the ligand with
CC the modulator under conditions such that the modulator binds to the
CC ligand, and thus alters the affinity of the ligand for the target
CC molecule. The method is useful for treating a number of disorders e.g.
CC infection, autoimmunity, tumours, inflammatory proliferative diseases and
CC hypoglycaemia. The present sequence is an aptamer which was used to
CC illustrate the method of the invention
XX
SQ Sequence 33 BP; 8 A; 10 C; 8 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 29; DB 7; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGACUAUACCGGCAAUCGUGCAUCCCC 29
||||||||||||||||||||||||||||||
Db 3 GGGGACUAUACCGGCAAUCGUGCAUCCCC 31

RESULT 4
ABN88504
ID ABN88504 standard; RNA; 96 BP.
XX
AC ABN88504;
XX
DT 19-AUG-2002 (first entry)
XX
DE Coagulation factor IXa binding/inhibiting RNA aptamer SEQ ID NO:17.
XX
KW RNA aptamer; identification; coagulation factor; angiopoietin; thrombin;
KW E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant;
KW cell proliferation; intimal hyperplasia; angiogenesis;
KW bypass graft surgery; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200226932-A2.
XX
PD 04-APR-2002.
XX
PF 26-SEP-2001; 2001WO-US030004.
XX
PR 26-SEP-2000; 2000US-0235654P.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Sullenger BA, Rusconi CP;
XX
DR WPI; 2002-479560/51.
XX
PT Novel RNA aptamers that selectively bind coagulation pathway factors, E2F
PT family members, Ang1 or Ang2, useful for modulating coagulation pathway
PT factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.
XX
PS Claim 13; Fig 1B; 216pp; English.
XX
CC The present invention describes RNA aptamers (I,II,III) that selectively
CC bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c)
CC angiopoietin-1 (Ang1) or Ang2, respectively, where (I), (II), (III) have
CC a dissociation constant for the coagulation pathway factor, an E2F family
CC member, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) have
CC cardiant and cytostatic activities. (I) are useful for modulating the
CC biological activity of a coagulation pathway factor which involves
CC administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that
CC the biological activity of the coagulation pathway factor in the warm-
CC blooded vertebrate is modulated. (I) are also useful for treating
CC cardiovascular diseases in the mammal. (II) are useful for modulating E2F
CC activity in a warm-blooded vertebrate. (III) are useful for modulating
CC Ang1 or Ang2 activity in a warm-blooded vertebrate. (I) are potent
CC anticoagulants and significantly delay the clotting time of normal human
CC plasma or the activation of platelets in response to thrombin. (II) are
CC useful for inhibiting cell proliferation in a number of conditions e.g.,
CC intimal hyperplasia following bypass graft surgery. (III) are useful for
CC modulating angiogenesis. The RNA aptamers are also useful for diagnostic,
CC research and therapeutic context. The aptamers are useful as diagnostic
CC reagents to detect the presence or absence of target substances to which
CC they specifically bind, and for identifying substances to which they
CC specifically bind, for isolating and purifying substances to which they
CC bind, and as a separation reagent for retrieving the targets to which
CC they specifically bind. ABN88488 to ABN88713 and ABB81231 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 96 BP; 28 A; 25 C; 28 G; 0 T; 15 U; 0 Other;

Query Match 100.0%; Score 29; DB 6; Length 96;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGACUAUACCGGCAAUCGUGCAUCCCC 29
||||||||||||||||||||||||||||||
Db 20 GGGGACUAUACCGGCAAUCGUGCAUCCCC 48

RESULT 5
AAT27772/c
ID AAT27772 standard; cDNA; 169 BP.
XX
AC AAT27772;
XX
DT 15-NOV-1996 (first entry)
XX
DE Human neural thread protein genomic clone (G5dPst-M13R).
XX
KW Neural thread protein; NTP; diagnosis; detection; Alzheimer's disease;
KW neuroectodermal tumour; malignant astrocytoma; monoclonal antibody;
KW binding fragment; ds.
XX
OS Homo sapiens.
XX
PN WO9615272-A1.
XX
PD 23-MAY-1996.
XX
PF 14-NOV-1995; 95WO-US017111.
XX
PR 14-NOV-1994; 94US-00340426.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI De La Monte S, Wands JR;
XX
DR WPI; 1996-259865/26.
XX
PT Detection of neural thread protein in diagnosis of Alzheimer's disease -
PT also NTP DNA and protein sequences used in gene and anti:sense therapy.
XX
PS Disclosure; Fig 22E; 238pp; English.
XX
CC A method for detecting the presence of neural thread protein (NTP) having
CC a molecular weight of 8, 14, 17, 21, 26 or 42 kD in a human subject
CC comprises (a) contacting a sample from a human subject that is suspected
CC of containing the NTP with at least one molecule capable of binding to
CC the protein; and (b) detecting any of the molecule bound to the protein.
CC The binding molecule is selected from an antibody free of natural
CC impurities, a monoclonal antibody or a binding fragment of either of
CC these. The method may be used for diagnosing the presence of Alzheimer's
CC disease, neuroectodermal tumours and a malignant astrocytoma in a human.
CC A number of clones of neural thread protein were isolated from healthy 17
CC -18 week old foetal human brain (HB) 2 year old temporal lobe neocortex

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CC   and end stage Alzheimer's disease (AD) cerebral cortex. See AAT27753-75
XX
SQ   Sequence 169 BP; 48 A; 24 C; 41 G; 56 T; 0 U; 0 Other;

  Query Match             65.5%;  Score 19;  DB 2;  Length 169;
  Best Local Similarity   70.4%;  Pred. No. 29;
  Matches   19;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 GGACUAUACCGGCAAUCGUGCAUCCCC 29
              |||| | | |||| |:||:|| :||||
Db         36 GGACCAAAGCGGCCATCGTGCCTCCCC 10


RESULT 6
ABN88494
ID   ABN88494 standard; RNA; 96 BP.
XX
AC   ABN88494;
XX
DT   19-AUG-2002  (first entry)
XX
DE   Coagulation factor IXa binding/inhibiting RNA aptamer SEQ ID NO:7.
XX
KW   RNA aptamer; identification; coagulation factor; angiopoietin; thrombin;
KW   E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant;
KW   cell proliferation; intimal hyperplasia; angiogenesis;
KW   bypass graft surgery; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200226932-A2.
XX
PD   04-APR-2002.
XX
PF   26-SEP-2001; 2001WO-US030004.
XX
PR   26-SEP-2000; 2000US-0235654P.
XX
PA   (UYDU-) UNIV DUKE.
XX
PI   Sullenger BA,  Rusconi CP;
XX
DR   WPI; 2002-479560/51.
XX
PT   Novel RNA aptamers that selectively bind coagulation pathway factors, E2F
PT   family members, Ang1 or Ang2, useful for modulating coagulation pathway
PT   factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.
XX
PS   Claim 13; Fig 1A; 216pp; English.
XX
CC   The present invention describes RNA aptamers (I,II,III) that selectively
CC   bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c)
CC   angiopoietin-1 (Ang1) or Ang2, respectively, where (I), (II), (III) have
CC   a dissociation constant for the coagulation pathway factor, an E2F family
CC   member, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) have
CC   cardiant and cytostatic activities. (I) are useful for modulating the
CC   biological activity of a coagulation pathway factor which involves
CC   administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that
CC   the biological activity of the coagulation pathway factor in the warm-
CC   blooded vertebrate is modulated. (I) are also useful for treating
CC   cardiovascular diseases in the mammal. (II) are useful for modulating E2F
CC   activity in a warm-blooded vertebrate. (III) are useful for modulating
CC   Ang1 or Ang2 activity in a warm-blooded vertebrate. (I) are potent
CC   anticoagulants and significantly delay the clotting time of normal human
CC   plasma or the activation of platelets in response to thrombin. (II) are
CC   useful for inhibiting cell proliferation in a number of conditions e.g.,
CC   intimal hyperplasia following bypass graft surgery. (III) are useful for
CC   modulating angiogenesis. The RNA aptamers are also useful for diagnostic,
CC   research and therapeutic context. The aptamers are useful as diagnostic
CC   reagents to detect the presence or absence of target substances to which
CC   they specifically bind, and for identifying substances to which they
CC   specifically bind, for isolating and purifying substances to which they
CC   bind, and as a separation reagent for retrieving the targets to which
CC   they specifically bind. ABN88488 to ABN88713 and ABB81231 represent
CC   sequences used in the exemplification of the present invention
XX
SQ   Sequence 96 BP; 24 A; 26 C; 30 G; 0 T; 16 U; 0 Other;

  Query Match             61.4%;  Score 17.8;  DB 6;  Length 96;
  Best Local Similarity   90.5%;  Pred. No. 1e+02;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 ACUAUACCGGCAAUCGUGCAU 25
              |||||||||| |||||||||
Db         30 ACUAUACCGGUCAUCGUGCAU 50


RESULT 7
AAX11804
ID   AAX11804 standard; DNA; 101 BP.
XX
AC   AAX11804;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Human biallelic polymorphic DNA fragment WI-18680.
XX
KW   Polymorphism; biallelic; human; forensic; paternity testing; disease;
KW   detection; phenotypic typing; characteristic; infection; hereditary;
KW   autoimmune disease; cancer; inflammation; drug; therapy; medicament;
KW   treatment; marker; ss.
XX
OS   Homo sapiens.
XX
PN   WO9820165-A2.
XX
PD   14-MAY-1998.
XX
PF   05-NOV-1997;   97WO-US020313.
XX
PR   06-NOV-1996;   96US-0030455P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Lander ES,  Wang D,  Hudson T;
XX
DR   WPI; 1998-286974/25.
XX
PT   New isolated nucleic acid segments from the human genome - used for
PT   determining polymorphic forms for use in e.g. forensics, paternity
PT   testing or phenotypic typing for disease.
XX
PS   Claim 1; Page 195; 310pp; English.
XX
CC   AAX10269-X12937 are human DNA fragments which contain biallelic
CC   polymorphic markers which have been isolated using the primers
CC   represented in AAX09121-X10268. The base occupying the polymorphic site
CC   is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments
CC   can be used in methods for determining polymorphic forms in an individual
CC   for use in e.g. forensics, paternity testing or for phenotypic typing for
CC   diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan
CC   syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease,
CC   familial hypercholesterolemia, polycystic kidney disease, hereditary
CC   spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary
CC   haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
CC   syndrome, osteogenesis imperfecta, acute intermittent porphyria,
CC   autoimmune diseases, inflammation, cancer, diseases of the nervous
CC   system, infection by pathogenic microorganisms, and characteristics such
CC   as longevity, appearance (e.g. baldness, obesity), strength, speed,
CC   endurance, fertility, and susceptibility or receptivity to particular
CC   drugs or therapeutic treatments. The isolated polymorphic nucleic acid
CC   segments can also be used to produce medicaments for the treatment or
CC   prophylaxis of such diseases
XX
SQ   Sequence 101 BP; 27 A; 23 C; 26 G; 24 T; 0 U; 1 Other;
```

```
  Query Match             61.4%;  Score 17.8;  DB 2;  Length 101;
  Best Local Similarity   62.1%;  Pred. No. 1e+02;
  Matches   18;  Conservative    4;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 GGGGACUAUACCGGCAAUCGUGCAUCCCC 29
              | | ||: :||  |||| | :|||:|||| 
Db         11 GAGTACTGTACACGCAAGCATGCATCCCC 39
```

RESULT 8
ADE35061
ID   ADE35061 standard; DNA; 166 BP.
XX
AC   ADE35061;
XX
DT   29-JAN-2004 (first entry)
XX
DE   Mouse fibroblast growth factor-4 promoter.
XX
KW   Fibroblast growth factor-4; FGF-4; mouse; stem cell; promoter; ds.
XX
OS   Mus sp.
XX
PN   WO2003080816-A2.
XX
PD   02-OCT-2003.
XX
PF   18-MAR-2003; 2003WO-GB001111.
XX
PR   19-MAR-2002; 2002GB-00006422.
PR   08-MAY-2002; 2002GB-00010458.
XX
PA   (UYSH-) UNIV SHEFFIELD.
XX
PI   Andrews P, Draper J;
XX
DR   WPI; 2003-779256/73.
XX
PT   Manipulating phenotype of stem cell by providing cell transfected with
PT   nucleic acid comprising promoter which confers substantial stem cell
PT   specific expression on selective marker gene(s), and proliferating cell.
XX
PS   Disclosure; Fig 2; 40pp; English.
XX
CC   The present sequence is that of the mouse fibroblast growth factor-3 (FGF
CC   -4) promoter from nucleotides -64 to +101. Transcription factor binding
CC   motifs ADE35058-ADE35060 from FGF-4 promoters have been shown to direct
CC   stem cell specific expression. This discovery was exploited in methods of
CC   the invention for manipulating the phenotype of a stem cell. In such a
CC   method, a cell is transfected with a nucleic acid molecule that includes
CC   a promoter which comprises a motif that confers stem cell specific
CC   expression on a selectable marker (e.g. fluorescent protein or prodrug
CC   activating polypeptide) gene, and conditions conducive to proliferation
CC   of the cell are provided. A cell culture system is provided which
CC   facilitates the maintenance of stem cells, particularly embryonic stem
CC   cells, in an undifferentiated state. Also provided are differentiated
CC   cells and tissues, the genome of which includes a nucleic acid construct
CC   comprising a promoter which has a stem cell specific expression pattern
CC   which controls expression of a gene the expression of which allows the
CC   selective ablation of cells which have de-differentiated to a stem cell
CC   phenotype, thereby allowing their removal from a population of
CC   differentiated cells. The stem cells are haematopoietic, neural, bone,
CC   muscle, mesenchymal, trophoblastic, epithelial, endodermal or embryonic
CC   stem cells (including embryonal carcinoma TERA2 or NTERA2 cells), or
CC   embryonal germ cells.
XX
SQ   Sequence 166 BP; 27 A; 57 C; 53 G; 29 T; 0 U; 0 Other;

```
  Query Match             57.9%;  Score 16.8;  DB 9;  Length 166;
  Best Local Similarity   60.7%;  Pred. No. 3.4e+02;
  Matches   17;  Conservative    4;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 GGGGACUAUACCGGCAAUCGUGCAUCCC 28
              ||||||:|: ||| ||    :|| :||| 
Db         67 GGGGACTATCCCGCCACCGTTGCGTCCC 94
```

RESULT 9
ADE35062
ID   ADE35062 standard; DNA; 181 BP.
XX
AC   ADE35062;
XX
DT   29-JAN-2004 (first entry)
XX
DE   Mouse fibroblast growth factor-4 promoter.
XX
KW   Fibroblast growth factor-4; FGF-4; mouse; stem cell; promoter; ds.
XX
OS   Mus sp.
XX
PN   WO2003080816-A2.
XX
PD   02-OCT-2003.
XX
PF   18-MAR-2003; 2003WO-GB001111.
XX
PR   19-MAR-2002; 2002GB-00006422.
PR   08-MAY-2002; 2002GB-00010458.
XX
PA   (UYSH-) UNIV SHEFFIELD.
XX
PI   Andrews P, Draper J;
XX
DR   WPI; 2003-779256/73.
XX
PT   Manipulating phenotype of stem cell by providing cell transfected with
PT   nucleic acid comprising promoter which confers substantial stem cell
PT   specific expression on selective marker gene(s), and proliferating cell.
XX
PS   Disclosure; Fig 2; 40pp; English.
XX
CC   The present sequence is that of the mouse fibroblast growth factor-3 (FGF
CC   -4) promoter from nucleotides -64 to +116. Transcription factor binding
CC   motifs ADE35058-ADE35060 from FGF-4 promoters have been shown to direct
CC   stem cell specific expression. This discovery was exploited in methods of
CC   the invention for manipulating the phenotype of a stem cell. In such a
CC   method, a cell is transfected with a nucleic acid molecule that includes
CC   a promoter which comprises a motif that confers stem cell specific
CC   expression on a selectable marker (e.g. fluorescent protein or prodrug
CC   activating polypeptide) gene, and conditions conducive to proliferation
CC   of the cell are provided. A cell culture system is provided which
CC   facilitates the maintenance of stem cells, particularly embryonic stem
CC   cells, in an undifferentiated state. Also provided are differentiated
CC   cells and tissues, the genome of which includes a nucleic acid construct
CC   comprising a promoter which has a stem cell specific expression pattern
CC   which controls expression of a gene the expression of which allows the
CC   selective ablation of cells which have de-differentiated to a stem cell
CC   phenotype, thereby allowing their removal from a population of
CC   differentiated cells. The stem cells are haematopoietic, neural, bone,
CC   muscle, mesenchymal, trophoblastic, epithelial, endodermal or embryonic
CC   stem cells (including embryonal carcinoma TERA2 or NTERA2 cells), or
CC   embryonal germ cells.
XX
SQ   Sequence 181 BP; 27 A; 63 C; 62 G; 29 T; 0 U; 0 Other;

```
  Query Match             57.9%;  Score 16.8;  DB 9;  Length 181;
  Best Local Similarity   60.7%;  Pred. No. 3.4e+02;
  Matches   17;  Conservative    4;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 GGGGACUAUACCGGCAAUCGUGCAUCCC 28
              ||||||:|: ||| ||    :|| :||| 
Db         67 GGGGACTATCCCGCCACCGTTGCGTCCC 94
```

```
RESULT 10
ABZ21255
ID   ABZ21255 standard; RNA; 29 BP.
XX
AC   ABZ21255;
XX
DT   16-APR-2003  (first entry)
XX
DE   FIXa aptamer, SEQ ID 15.
XX
KW   Immunosuppressive; aptamer; infection; autoimmunity; tumour;
KW   inflammatory proliferative disease; hypoglycaemia; human;
KW   coagulation Factor IXa; FIXa; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1. .5
FT                   /*tag=  a
FT                   /bound_moiety= "Nucleotides 25. .29"
FT   stem_loop       11. .21
FT                   /*tag=  b
FT   misc_binding    25. .29
FT                   /*tag=  c
FT                   /bound_moiety= "Nucleotides 1. .5"
XX
PN   WO200296926-A1.
XX
PD   05-DEC-2002.
XX
PF   28-MAY-2002; 2002WO-US016555.
XX
PR   25-MAY-2001; 2001US-0293231P.
PR   07-NOV-2001; 2001US-0331037P.
XX
PA   (UYDU-) UNIV DUKE.
XX
PI   Sullenger BA,  Rusconi C;
XX
DR   WPI; 2003-140438/13.
XX
PT   Altering affinity of nucleic acid ligands for target molecules in a
PT   patient or reversing binding of labeled ligands to target tissues, by
PT   administering (to a patient receiving the ligand) a modulator that binds
PT   to ligand.
XX
PS   Example 2; Fig 7; 111pp; English.
XX
CC   The present invention relates to a method for altering the affinity of a
CC   nucleic acid ligand (e.g. an aptamer) for a target molecule in a patient
CC   or in vitro, or reversing the binding of the labelled ligand to a target
CC   tissue. The method comprises administering a modulator that binds to the
CC   ligand to a patient receiving the ligand, or contacting the ligand with
CC   the modulator under conditions such that the modulator binds to the
CC   ligand, and thus alters the affinity of the ligand for the target
CC   molecule. The method is useful for treating a number of disorders e.g.
CC   infection, autoimmunity, tumours, inflammatory proliferative diseases and
CC   hypoglycaemia. The present sequence is an aptamer to human coagulation
CC   Factor IXa (FIXa aptamer), which was used to illustrate the method of the
CC   invention
XX
SQ   Sequence 29 BP; 8 A; 8 C; 8 G; 0 T; 5 U; 0 Other;

  Query Match             55.9%;  Score 16.2;  DB 7;  Length 29;
  Best Local Similarity   72.4%;  Pred. No. 5.1e+02;
  Matches   21;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 GGGGACUAUACCGGCAAUCGUGCAUCCCC 29
              |||||||||||  | |    ||||||| |
Db          1 GGGGACUAUACGUGAACGACUGCAUCCAC 29


RESULT 11
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```
ABN88499
ID   ABN88499 standard; RNA; 95 BP.
XX
AC   ABN88499;
XX
DT   19-AUG-2002  (first entry)
XX
DE   Coagulation factor IXa binding/inhibiting RNA aptamer SEQ ID NO:12.
XX
KW   RNA aptamer; identification; coagulation factor; angiopoietin; thrombin;
KW   E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant;
KW   cell proliferation; intimal hyperplasia; angiogenesis;
KW   bypass graft surgery; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200226932-A2.
XX
PD   04-APR-2002.
XX
PF   26-SEP-2001; 2001WO-US030004.
XX
PR   26-SEP-2000; 2000US-0235654P.
XX
PA   (UYDU-) UNIV DUKE.
XX
PI   Sullenger BA,  Rusconi CP;
XX
DR   WPI; 2002-479560/51.
XX
PT   Novel RNA aptamers that selectively bind coagulation pathway factors, E2F
PT   family members, Ang1 or Ang2, useful for modulating coagulation pathway
PT   factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.
XX
PS   Claim 13; Fig 1A; 216pp; English.
XX
CC   The present invention describes RNA aptamers (I,II,III) that selectively
CC   bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c)
CC   angiopoietin-1 (Ang1) or Ang2, respectively, where (I), (II), (III) have
CC   a dissociation constant for the coagulation pathway factor, an E2F family
CC   member, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) have
CC   cardiant and cytostatic activities. (I) are useful for modulating the
CC   biological activity of a coagulation pathway factor which involves
CC   administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that
CC   the biological activity of the coagulation pathway factor in the warm-
CC   blooded vertebrate is modulated. (I) are also useful for treating
CC   cardiovascular diseases in the mammal. (II) are useful for modulating E2F
CC   activity in a warm-blooded vertebrate. (III) are useful for modulating
CC   Ang1 or Ang2 activity in a warm-blooded vertebrate. (I) are potent
CC   anticoagulants and significantly delay the clotting time of normal human
CC   plasma or the activation of platelets in response to thrombin. (II) are
CC   useful for inhibiting cell proliferation in a number of conditions e.g.,
CC   intimal hyperplasia following bypass graft surgery. (III) are useful for
CC   modulating angiogenesis. The RNA aptamers are also useful for diagnostic,
CC   research and therapeutic context. The aptamers are useful as diagnostic
CC   reagents to detect the presence or absence of target substances to which
CC   they specifically bind, and for identifying substances to which they
CC   specifically bind, for isolating and purifying substances to which they
CC   bind, and as a separation reagent for retrieving the targets to which
CC   they specifically bind. ABN88488 to ABN88713 and ABB81231 represent
CC   sequences used in the exemplification of the present invention
XX
SQ   Sequence 95 BP; 25 A; 26 C; 29 G; 0 T; 15 U; 0 Other;

  Query Match             55.9%;  Score 16.2;  DB 6;  Length 95;
  Best Local Similarity   72.4%;  Pred. No. 6.1e+02;
  Matches   21;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 GGGGACUAUACCGGCAAUCGUGCAUCCCC 29
              |||||||||||  | |    ||||||| |
Db         20 GGGGACUAUACGUGAACGACUGCAUCCAC 48
```

RESULT 12
ABX91389
ID ABX91389 standard; cDNA; 172 BP.
XX
AC ABX91389;
XX
DT 07-MAY-2003 (first entry)
XX
DE Murine gene trapped sequence (GTS) SEQ ID No 733.
XX
KW Murine; mouse; gene trap technology; gene trapped sequence; GTS;
KW gene identification; functional genomic analysis; gene discovery;
KW gene expression analysis; cross species hybridisation analysis;
KW antisense inhibition; gene targeting; gene; ss.
XX
OS Mus sp.
XX
PN US2002161207-A1.
XX
PD 31-OCT-2002.
XX
PF 30-NOV-2000; 2000US-00728444.
XX
PR 01-DEC-1999; 99US-0168360P.
XX
PA (FRIE/) FRIEDRICH G.
PA (ZAMB/) ZAMBROWICZ B.
PA (SAND/) SANDS A T.
XX
PI Friedrich G, Zambrowicz B, Sands AT;
XX
DR WPI; 2003-288124/28.
XX
PT New murine polynucleotides comprising gene trapped sequences, useful in
PT functional genomic analysis, in the development of new therapeutic or
PT diagnostic agents, for diagnostic gene expression analysis or for genetic
PT manipulations.
XX
PS Claim 2; SEQ ID NO 733; 29pp; English.
XX
CC The present invention relates to novel murine cDNAs produced using gene
CC trap technology. The OMNIBANK gene trapped sequences (GTSs) are
CC individually identified novel genes, and are useful in functional genomic
CC analysis, in the discovery and development of new therapeutic and
CC diagnostic agents, for gene discovery, for diagnostic gene expression
CC analysis, for cross species hybridisation analysis, and for genetic
CC manipulations such as antisense inhibition or gene targeting. The
CC polynucleotides of the invention are also useful for isolating cDNAs,
CC genomic clones or full-length genes/polynucleotides, or their homologues,
CC heterologues, paralogues or orthologues, that are capable of hybridising
CC to one or more of the new murine polynucleotide sequences. The
CC polynucleotides are also useful for identifying the coding regions of the
CC murine genome, and as hybridisation probes. ABX90657-ABX91862 represent
CC the murine GTSs of the invention. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ Sequence 172 BP; 51 A; 53 C; 38 G; 26 T; 0 U; 4 Other;

Query Match 55.2%; Score 16; DB 7; Length 172;
Best Local Similarity 60.0%; Pred. No. 8.3e+02;
Matches 15; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

```
Qy          3 GGACUAUACCGGCAAUCGUGCAUCC 27
              |||  |:|||  || :| :|||:||
Db         90 GGANGATACCTTCAGTCCTGCATCC 114
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RESULT 13
ABZ01528/c
ID ABZ01528 standard; DNA; 50 BP.
XX
AC ABZ01528;
XX
DT 09-JAN-2003 (first entry)
XX
DE Human leukocyte gene expression profiling probe SEQ ID NO 1519.
XX
KW T7; leukocyte; gene expression profiling; allograft rejection;
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200257414-A2.
XX
PD 25-JUL-2002.
XX
PF 22-OCT-2001; 2001WO-US047856.
XX
PR 20-OCT-2000; 2000US-0241994P.
PR 08-JUN-2001; 2001US-0296764P.
XX
PA (BIOC-) BIOCARDIA INC.
XX
PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
PI Ly N, Woodward R, Quertermous T, Johnson F;
XX
DR WPI; 2002-636525/68.
XX
PT New system for leukocyte expression profiling, diagnosing a disease, or
PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
PT or congestive heart failure, comprises diagnostic oligonucleotides.
XX
PS Claim 1; Page 374; 0pp; English.
XX
CC The invention relates to a system for detecting gene expression, which
CC comprises one or two isolated DNA molecules that detect expression of a
CC gene, where the gene corresponds to any of 8143 oligonucleotides
CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
CC for leukocyte expression profiling. It is particularly useful for
CC diagnosing a disease, monitoring (rate of) progression of a disease,
CC predicting therapeutic outcome, determining prognosis for a patient,
CC predicting disease complications in an individual or monitoring response
CC to treatment in an individual. The diseases include cardiac allograft
CC rejection, kidney allograft rejection, liver allograft rejection,
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX
SQ Sequence 50 BP; 8 A; 8 C; 15 G; 19 T; 0 U; 0 Other;

Query Match 54.5%; Score 15.8; DB 6; Length 50;
Best Local Similarity 63.0%; Pred. No. 8.7e+02;
Matches 17; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

```
Qy          3 GGACUAUACCGGCAAUCGUGCAUCCCC 29
              |||| |:| | ||||:   |||:| ||
Db         37 GGACCATATCAGCAATGAGGCATCACC 11
```

RESULT 14
ADA01911/c
ID ADA01911 standard; DNA; 105 BP.
XX
AC ADA01911;
XX
DT 06-NOV-2003 (first entry)
XX
DE Mouse carcinoma associated nucleic acid, SEQ ID NO:430.
XX
KW Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast;
KW prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
KW ds.

XX
OS Mus sp.
XX
PN WO2003057146-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041414.
XX
PR 26-DEC-2001; 2001US-00035832.
XX
PA (SAGR-) SAGRES DISCOVERY.
XX
PI Morris DW;
XX
DR WPI; 2003-587068/55.
XX
PT New recombinant nucleic acid encoding carcinoma associated protein,
PT useful for preparing compositions for treating carcinomas.
XX
PS Claim 1; Page 185; 245pp; English.
XX
CC The invention relates to recombinant carcinoma associated (CA) nucleic
CC acid sequences from mouse and human (ADA01482-ADA03094), and to
CC recombinant carcinoma associated proteins (CAP) encoded by them. The
CC invention also encompasses expression vectors and host cells comprising a
CC CA nucleic acid, a polypeptide (especially an antibody) that specifically
CC binds to the protein, and a biochip comprising CA nucleic acid or
CC fragments thereof. The sequences of the invention were identified using
CC oncogenic retroviruses, which insert into the genome of the host organism
CC at random. Many of these do not carry transduced host oncogenes or
CC pathogenic trans-acting viral genes, meaning that cancer incidence is a
CC direct consequence of the effects of proviral integration into host
CC protooncogenes. The CA nucleic acid sequences can be used to diagnose
CC carcinoma (especially breast cancer, prostate cancer, lymphoma or
CC leukaemia) or a propensity to carcinoma by determination of the sequence
CC of a CA gene, or by determination of CA gene expression in particular
CC tissues. CA nucleic acids, proteins and antibodies are also useful as
CC therapeutic agents and in screening and evaluating drug candidates. The
CC present sequence represents a specifically claimed murine CA nucleic acid
CC sequence of the invention. Note: The sequence data for this patent is
CC also available in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 105 BP; 34 A; 21 C; 29 G; 21 T; 0 U; 0 Other;

Query Match 54.5%; Score 15.8; DB 8; Length 105;
Best Local Similarity 73.7%; Pred. No. 9.7e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGACUAUACCGGCAAUCG 20
|| ||:|:|| |||||:||
Db 27 GGTACTATACTGGCAATCG 9

RESULT 15
ADB71650/c
ID ADB71650 standard; DNA; 105 BP.
XX
AC ADB71650;
XX
DT 04-DEC-2003 (first entry)
XX
DE Mouse carcinoma associated gene fragment #430.
XX
KW mouse; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;
KW cancer; neoplasm; adenocarcinoma; sarcoma.
XX
OS Mus sp.
XX
PN WO2003008583-A2.
XX
PD 30-JAN-2003.
XX
PF 26-DEC-2001; 2001WO-US051291.
XX
PR 02-MAR-2001; 2001US-00798586.
PR 23-OCT-2001; 2001US-00004113.
PR 08-NOV-2001; 2001US-00052482.
PR 30-NOV-2001; 2001US-00997722.
PR 20-DEC-2001; 2001US-00034650.
XX
PA (SAGR-) SAGRES DISCOVERY.
XX
PI Morris DW, Engelhard EK;
XX
DR WPI; 2003-239337/23.
XX
PT New recombinant nucleic acid, useful for treating carcinomas, lymphomas,
PT cancers, neoplasm, adenocarcinoma, or sarcomas.
XX
PS Claim 1; Page 144; 2304pp; English.
XX
CC The invention relates to a novel recombinant nucleic acid comprising a
CC nucleotide sequence selected from any of the 660 sequences fully defined
CC in the specification. A polynucleotide of the invention has cytostatic
CC activity, and may have a use in gene therapy, or in a vaccine. The
CC recombinant nucleic acids and polypeptides are useful for treating
CC carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and
CC sarcomas. The sequences shown in ADB71221-ADB72172 represent mouse
CC sequence tags, or genomic insertion sites, of carcinoma associated (CA)
CC genes of the invention.
XX
SQ Sequence 105 BP; 34 A; 21 C; 29 G; 21 T; 0 U; 0 Other;

Query Match 54.5%; Score 15.8; DB 9; Length 105;
Best Local Similarity 73.7%; Pred. No. 9.7e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGACUAUACCGGCAAUCG 20
|| ||:|:|| |||||:||
Db 27 GGTACTATACTGGCAATCG 9

Search completed: April 9, 2004, 03:17:48
Job time : 105.035 secs